

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Anish Gupta

Location: rem/3A59/3C18

Art Unit: 1654

Friday, May 12, 2006

Case Serial Number: 09/759584

From: Toby Port

Location: Biotech-Chem Library

REM-1A59

Phone: (571)272-2523

toby.port@uspto.gov

Searon Noises

Dear Examiner Gupta,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port Technical Information Specialist STIC Biotech/Chem Library (571)272-2523



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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

/ 0.	untary Results Feedback Form
>	I am an examiner in Workgroup: Example: 1610
. >	Relevant prior art found, search results used as follows:
	☐ 102 rejection
•	☐ 103 rejection
	☐ Cited as being of interest.
	☐ Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Co	omments:

Top off or send completed forms to SIIIC-Biotech-Chem Library. Remsen Bldg





ME

STIC-Biotech/ChemLib

1885//

From:

Gupta, Anish

Sent: To: Wednesday, May 03, 2006 2:14 PM

To: Subject: STIC-Biotech/ChemLib SEARCH REQUEST

Search Request:

Name: Anish Gupta Examiner #: 73121

date: 5-3-06' Art Unit: 1654 Phone # 2-965

Serial Number 09/759584

Location: 3A59 Mailbox #: 3C18

Please search the nucleic acid encoding the protein of SEQ ID NO 49, SEQ ID NO 59 and SEQ ID NO 48.

thank you

anish gupta

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#_____ AA#:____

S/L:___ Oligomer:____

Encode/Transl:____

Structure #:____Text:___

Inventor:____ Litigation:___

Vendors and cost where applicable STN:
DIALOG:
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Other (Specify):

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1 (Dases 1 to 414)

Broeksert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.C. and Vanderleyden, J.

Biocidal proteins
Patent: US 5824869-A 48 20-OCT-1998;

Location/Qualifiers
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tive 0; Mismatches 0;
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PALENT: WO 9721814-A 19 19-JUN-1997;
ZENECA LTD (GB)
Other publication AU 1105397 19970703.
Location/Qualifiers
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100.0%; Score 414; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.4e-82;
Matches 414; Conservative 0; Mismatches 0;
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Location/Qualifiers

    .414
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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Sequence 37 from Patent WO9416076.
A39549
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Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, P.R.G. and Vanderleyden, J.
Blocidal proteins
Patent: US 5538525-A 48 23-JUL-1996;
Location/Qualifiers
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Sequence 48 from patent US 5538525.
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1 (bases 1 to 414)
Broskaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Blocidal proteins
Patent: US 6187904-A 48 13-FEB-2001;
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Sequence 48 from patent US 6187904.
AR130272.1 GI:14118169
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Matches 414; Conservative 0
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DEFINITION ACCESSION VERSION KEYWORDS

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Rees, S.B., De Samblanx, G.W. and Broekaert, W.F.
Antifungal proteins
Patent: US 6864068-A 19 08-MAR-2005;
Syngenta Limited; Guilford;
GBX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 414; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.4e-82;
Matches 414; Conservative 0; Mismatches 0;
                                            Score 414; DB 6;
Pred. No. 1.4e-82;
; Mismatches 0;
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Sequence 19 from patent US 6864068.
AR642703.1 GI:62779939
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/mol_type="genomic DNA
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                                                                                                                          Unclassified.

1 (bases 1 to 414)
De Samblanx, G.Wivina., Broekaert, W.Frans. and Rees, S.Bronwen. Antifungal proteinly preteint 19 16-APR-2002;
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Van Amerongen, A., Fant, F., Borrremans, F.A., De Samblanx, G.W.,

Sijtsma, L., Meloen, R.H., Puijk, W.C., Schaaper, W.M.M.,

Broekkaer, W.F., van Gelder, W.M.J. and Rees, S.B.

Antifungal peptides and composition thereof

Patent: US 6605698-A 45 12-AUG-2003;

Syngenta Limited; Guildford;
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Best Local Similarity 100.0%; Pred. No. 1.4e-82;
Matches 414; Conservative 0; Mismatches 0;
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           414 bp I
Sequence 19 from patent US 6372888.
AR207337
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    414
    organism="unknown"

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                                                                GI:21506219
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Unclassified.
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REFERENCE AUTHORS

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Shoji.K.
Phage and plasmid constructed by ligating antibacterial protein gene DNA with vector DNA, transformant microorganism and transformant plant containing the same and antibacterial protein patent: JP 200116379-A 1 25-APR-2000;
TOYAWA PREF
OS Rephanus sativus L.
PN JP 200116379-A/1
PD 25-APR-2000
PP 09-OCT-1998 JP 1998288472
PR 09-OCT-1998 JP 1998288472
PR PO-OCT-1998 JP 1998288472
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C12N15/09,A01H5/00,A01N65/00,C07K14/415,C12N1/21,C12N5/10// PC
(C12N15/09,C12R1:91),(C12N1/21,C12R1:19),(C12N5/10,C12R1:91), PC
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Key Location/Qualifiers
Fource Location/Qualifiers
fource | 1.949
                                                                                                                                                         Length 395;
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                                                                                                                                                       95.2%; Score 394; DB 15;
100.0%; Pred. No. 4.5e-78;
iive 0; Mismatches 0;
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E34290.1 GI:18624295
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sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /guncion=antifungal, fungistatic"
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                                                                                                                                                                                                                                                                                                                                                                                                RSU18557 1395 bp mRNA linear PLN 07-JUL-1995 Raphanus sativus antifungal protein 1 preprotein (Rs-AFP1) mRNA,
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Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
On Feb 9, 1995 this sequence version replaced gi:609321.
Location/Qualifiers
                                                                                                                 241 IGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTTATGTAATTTAC 300
                                                                                                                                                                                             181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                                                                                                                                                        301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
                                                                                        241 IGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC
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/mol_type="mRNA"
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1:395_type="seed"
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Raphanus sativus
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102. .254
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PAT 16-MAY-2001
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                                                                                             181 AACCTIGAGAAAGCACGACAIGGATCTIGCAACTAIGTCTTCCCAGCTCACAAGTGIAIC 240
208 AGACTIGAGAAAGCACGACAIGGAICTIGCAACIAIGICTICCCAGCICACAAGIGIAIC 267
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88 GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCCAAAGG 147
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Unclassified.
1 (Dases 1 to 288)
Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
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Unclassified.
Unclassified.
1 (bases 1 to 288)
1 (bases 1 to 288)
Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 5824869-A 58 20-OCT-1998;
Location/Qualifiers
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Sequence 58 from patent US 6187904.
AR130280 GI:14118177
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Sequence 58 from patent US 5824869.
AROSO161. GI:5972153
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Matches 256; Conservative
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unclassified sequences.
1 (bases 1 to 288)
Dubock,A.C., Powell,K.A. and Rees,S.B.
ANTIMICROBIAL-PROTRIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
Patent: WO 9416076-A 41 21-JUL-1994;
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Pred. No. 1.1e-46;
0; Mismatches 3;
                                                                                                                Score 255; DB 6;
Pred. No. 6.9e-47;
0; Mismatches 74
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Location/Qualifiers
1. .288
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 Location/Qualifiers
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Sequence 41 from Patent WO9416076.
A39553.
A39553.1 GI:2295844
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Best Local Similarity 98.8%;
Matches 256; Conservative C
                                                                                                                Query Match 61.6%;
Best Local Similarity 81.0%;
Matches 333; Conservative (
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Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 5538525-A 58 23-JUL-1996;
Location/Qualifiers
                                                                                                                                                     Length 288;
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                                                                                                                                                                                                                     1 GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTT
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Terras, F.R.G. and Vanderleyden, J.
Blockdal proteins
Patent: US 6187904-A 58 13-PEB-2001;
Location/Qualifiers
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Sequence 58 from patent US 5538525.
123736 131:1603606

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    /mol_type="unassigned DNA"

                                                                               /organism="unknown"
/wol_type="unassigned DNA"
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Search completed: May 10, 2006, 05:29:30 Job time : 2310 secs

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May 10, 2006, 01:08:52 ; Search time 672 Seconds (without alignments) 4105.927 Million cell updates/sec
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Biocceleration Ltd.
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GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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11. geneseqn1980s:*
22. geneseqn1990s:*
43. geneseqn2000s:*
54. geneseqn2001as:*
55. geneseqn2001as:*
66. geneseqn2002as:*
67. geneseqn2002as:*
68. geneseqn2003as:*
69. geneseqn2003as:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    geneseqn2004as:*geneseqn2004bs:*geneseqn2005s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      geneseqn2003cs:*
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                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
               Copyright
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Perfect score:
                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                       Searched:
                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Location/Qualifiers 16. .256 /*tag= a

Raphanus sativus.

Key

	Description	Aaq38650 Rs-AFP1 C	Aaq70128 Antimicro	Aat72333 Raphanus	Aat68696 Radish an	Adc51221 Brassica	Adu71300 Brassica	Adc51223 Brassica	Adu71302 Brassica	Aaa53190 Raphanus	Aaq38652 RB-AFP2 C	Aaq70130 Antimicro	Aav10632 A. thalia	Aaz99339 DNA encod	Aav10633 A. thalia	Adz75091 Arabidops	Aat94581 Composite	Aaz39123 Wasabia j	Aaz39124 Wasabia	Abq82690 Wasabia j
SUMMARIES	QI .	AAQ38650	AAQ70128	AAT72333	AAT68696	ADC51221	ADU71300	ADC51223	ADU71302	AAA53190	AAQ38652	AAQ70130	AAV10632	AAZ99339	AAV10633	ADZ75091	AAT94581	AAZ39123	AAZ39124	ABQ82690
	DB	8	7	7	α	10	13	10	13	٣	~	~	7	ю	7	7	7	٣	٣	9
	Query Match Length DB	414	414	414	414	394	394	426	426	449	261	288	403	575	400	400	200	414	416	243
de	Query Match	100.0	100.0	100.0	100.0	78.2	78.2	74.3	74.3	61.6	61.4	61.4	58.6	56.1	53.9	53.9	49.1	48.9	48.6	48.3
	Score	414	414	414	414	323.8	323.8	307.8	307.8	255	254.2	254.2	242.4	232.4	223	223	203.4	202.6	201	199.8
	Result No.	-	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial diseases.

Terras FRG;

Rees SB,

Cammue BPA, Osborn RW,

WPI; 1993-100978/12.

Broekaert WF, (Vanderleyden J;

(ICIL) IMPERIAL CHEM IND PLC.

91GB-00018523. 92GB-00003038. 92GB-00013526.

29-AUG-1991; 13-FEB-1992; 25-JUN-1992;

92WO-GB001570.

27-AUG-1992;

WO9305153-A1 18-MAR-1993.

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N	0			48.3	243	9	ADG87728	
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7	۳	98.2		47.9	243	φ	ABQ82691	-
7		9.96			243	ø	ABZ14241	Arabidop
7		9.96		47.5	243	ø	ADG87651	
7		196.6		47.5	243	9	ADG87824	Ä
~		196.6			243	æ	ABZ42136	
6	-	194.6		47.0	308	~	AAT94577	Aat94577 Cloned 5'
7	٦	93.8		46.8	481	~	AAT99289	-
3	0	180		43.5	270	~	AAT94582	
e		178.8		43.2	286	7	AAT94574	-
3		178		13.0	1973	m	AAC46924	-
٣		156.8		37.9	522	ო	AAZ99324	Aaz99324 DNA encod
e		154.2		37.2	534	٣	AAZ99327	DNA
		53.6		37.1	909	m	AAZ99326	DNA
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9		52.4		36.8	534	m	AA251396	Aaz51396 Portion o
6		152.4		36.8	534	m	AAZ99325	-
9	-	51.4			485	m	AAZ99333	Aaz99333 DNA encod
4	_	47.6		35.7	443	m	AAZ99330	O DNA
4	-	45 B		ď	485		AA299337	DNA
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AAQ38650 ID AAQ	650 AAQ38650	550	star	standard;	DNA;	414	BP.	
	•							
•	AAQ38650	550;						
	25-MA	2-20	003	(rev	(pea			
	07-JUL-1993	L-19	93	(fire	(first entry)	3		
	Rs-AFP1		CDNA.					
₹ }	Ranhaniig	81.10	100	satistie.		(Brassica: Arabidonsis: Cnicus: I.	Lathyria. Cliforia.
	fungic	ide	; ba	acter:	locide;	ania		gram positive;
	plant	die	ease	e res:	disease resistance;	ĭ	· · ·	

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TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
                                                                                                                                                                                                                                                                                                                                                                                             Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Ra-AFPI from R. sativus. The full-length CDNA sequence of Rs-AFPI is given in AAQ70128. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antifungal protein; candida; fungal resistance; food additive; radish;
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                                                                                                                                                                                                                                                                  Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 414; DB 2; Length 4
100.0%; Pred. No. 6e-92;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 31; 39pp; English
                                                                                                                                                               SB)
                                       94WO-GB000012.
                                                                              93GB-00000281.
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(first entry)
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Best Local Similarity 100.
Matches 414; Conservative
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                                                                                                                                                                                                       WPI; 1994-249223/30.
P-PSDB; AAR57325.
                                                                                                                        (ZENE ) ZENECA LTD
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                                       05-JAN-1994;
21-JUL-1994.
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19-JAN-1998
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                                This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a class product, which was further reamplified with the same primers and digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ product. This was used to screen a lambda ZAPII cDNA library by in situ product. This was used to screen a lambda capilitied and subjected to two additional screening rounds with the same probe. Inserts by in situ vivo into the pBluescript phagemid form with the aid of halper phage that size compared by agarces gel electrophoresis. Four clones had insert sizes of approx. 400bp the others between 250-300bp. The inserts confirm of their sequenced and found to differ only in the length of their 5, and 3, UTN's. The longest sequence is given here. (Updated on 25-MAR-2003 to correct PN field.)
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21; Fig 35; 110pp; English
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Matches 414; Conservative 0
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Length 414;

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                                                              241 IGCTACTITICCTIGITAATITATCGCAAACTCTITGGTGAATAGTITITATGTAATITAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA clone codes for the preprotein for radish antifungal protein 1 (RB-AFP1) (AAW19617). Novel antifungal proteins are based on Rs-AFP1, Rs-AFP2 (see AAW19616), Rs-AFP3 and Rs-AFP4, especially those in which Gly9 is repaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW26371-90) of Rs-AFP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly
                                                                                                                  ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
                                                                                                                                                                                             RB-AFP1; radish antifungal protein 1; fungicide; salt tolerance;
preservative; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 414;
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/transl except= (pos:85. .87, aa:Glu)
16. .102
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Radish antifungal protein 1 (Rs-AFP1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 2; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                  AAT68696 standard; cDNA; 414
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103. .255
/*tag= c
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Matches 414; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16. .258
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P-PSDB; AAW19617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raphanus sativus.
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                                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This cDNA sequence encodes an Rhapanus sativus (radish) antifungal protein (Rs-AFP1). Analogues of the homologous protein, Rs-AFP2 (AAM19281), have also been produced (see AAM19282-92, AAM19284-98, AAM19301-04, AAM1930-34 and AAM31765-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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crop protection; plant defensin; bacterial protection; preservative; ss
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Samblanx GW, Fant F, Borremans FAM, Rees SB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                     (pos:85. .87, aa:Glu)
                                                                                                                                                                                                                                 /product= "antifungal_protein_1"
                                                                        Location/Qualifiers
16. .258
                                                                                                                                       except=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig 2; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         95GB-00025455
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16. 102
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103. .255
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P-PSDB; AAW19280.
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                                      Raphanus sativus
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Van Gelder WMJ;
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28-MAR-1996;
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GTCACTATCAATGAGTGATTTTATGACATGTACCTGATATGTTATGTTGGTTCGGTTATA 360
sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Brassica oleracea defensin protein - SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTATGTTTGGTTCGGTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                               61 Crccaagcaccaacaaregregaagcacacagaagrrereccaagaccaagregaacares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                         76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGBAAGGCCAAGTGGGACATGG
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                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                       Length 394;
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                                                                                                                                                                           Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
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3.8e-70;
37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica oleracea defensin protein coding sequence
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                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                     Score 323.8;
Pred. No. 8.8
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                                                                                                                                                                                                                  lery Match 78.2%; set Local Similarity 90.4%; tches 357; Conservative
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/*tag=
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Best Local &
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                                   GTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCGCACTTCTTTTTGCTGCTCTT
                                                                                                                                                                                                                                                                   AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
                                                                                              GTTCTTTTTGCTGCTTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
                                                                                                                                                                               CCAAGIGGGACAIGGICAGGAGICTGIGGAAACAAIAACGCAIGCAAGAAICAGIGCAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antimicrobial protein; defensin; transgenic plant; composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea defensin protein coding sequence
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P-PSDB; ADC51222.
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Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCACTATCAATGAGTGATTTTATGACATGTACCTGATATATGTTATGTTGGTTCGGTTA 360
                                                                                                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica antimicrobial protein coding sequence - SEQ
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                                                                                                                             (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 307.8; DB 1:
Pred. No. 7.6e-66;
0; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antimicrobial; plant disease resistance; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTT
                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 3; 34pp; Japanese
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                                                                                   18-SEP-2001; 2001JP-00283117
                                            18-SEP-2001; 2001JP-00283117
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                                                                                                                                                                     WPI; 2003-621123/59.
P-PSDB; ADC51224.
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    25-MAR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                            75
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                                       Novel Brassica sp. derived protein having antimicrobial activity, useful for producing multiple disease resistant plants.
                                                                                                                                            The invention comprises the amino acid and coding sequence of an antimicrobial protein obtained from Brassica sp. The DNA and protein sequences of the invention are useful in the production of a multiple disease resistant plant. The present cDNA sequence encodes the Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATTTGCTACTTCCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCCAAGTGGGACATGG
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                                                                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                                                                    Score 323.8; DB 13; Length 394;
Pred. No. 8.8e-70;
0; Mismatches 37; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 composite disease resistance; pathogenic bacteria; rice white lasf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                            Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Brassica defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antimicrobial protein; defensin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica defensin protein coding sequence.
                                                                                                     Example 2; SEQ ID NO 1; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .243
/*tag= a
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                                                                                                                                                                                                                                                                                                                 Query Match 78.2%;
Best Local Similarity 90.4%;
Matches 357; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC51223 standard; DNA; 426
                                                                                                                                                                                                                                  oleracea defensin protein.
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P-PSDB; ADU71301
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ADC51223

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Brassica

Brassica

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64 CITITIGCIGCITICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCA 123
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                                  Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAAC 183
                                                                                                                                                                                                                                                                                                                                                                                                  Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and rice blast disease against pathogenic microbes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 TTAGTAGTGATCATGGCTAAGTTTGCTTCCATCATTGTCCTTCTCTTCGCTGCTTCTTTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 TACTTTCCTTGTTAATT-TATCGCAAACTCTTTGGTGAATAGTTT--TTATGTAATTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAAAATAAGTCAGTGACTATCCATGAGTGATTTTAAGACATGTACCAGATATG-TTA
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                                                                  paddy; radishin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 255; DB 3; Length 449;
Pred. No. 7.4e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
                                                                  Raphanus sativus, antibacterial, plant, resistance, pathogenic microbe, radish, rice blast disease, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 4; 7pp; Japanese.
                                                                                                                                                                                                                                     98JP-00288472
                                                                                                                                                                                                                                                                         98JP-00288472
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Best Local Similarity 81.0%;
Matches 333; Conservative (
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(first entry)
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-389821/34
                                                                                                                                                                                                                                                                                                             (TOYA-) TOYAMA KEN
                                                                                                                             Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY91117
                                                                                                                                                               JP2000116379-A
 06-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                               Novel Brassica sp. derived protein having antimicrobial activity, useful for producing multiple disease resistant plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises the amino acid and coding sequence of an antimicrobial protein obtained from Brassica sp. The DNA and protein sequences of the invention are useful in the production of a multiple disease resistant plant. The present DNA sequence encodes the Brassica antimicrobial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATTTGCTACTTCCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAACTTATGCGCAAACTCTTTGGTGGTTAGTTTTGTGTAATTTACATAAAATAAGTCTGT
                                                                                                          ID 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                           "Brassica antimicrobial protein - SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 74.3%; Score 307.8; DB 13; Best Local Similarity 88.8%; Pred. No. 7.6e-66; Matches 356; Conservative 0; Mismatches 42;
                                                                                                                                                                                                                                                                                            (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                   Location/Qualifiers
1. .243
/*tag= a
/product= "Brassica a
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 3; 16pp; Japanese
                                                                                                                                                                                                                    07-JUN-2004; 2004JP-00168986
                                                                                                                                                                                                                                                        18-SEP-2001; 2001JP-00283117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA53190 standard; DNA; 449
                                                                                                                                                                                                                                                                                                                              WPI; 2004-809169/80.
P-PSDB; ADU71303.
                                                                                                                                              JP2004329215-A
                      ďβ
                                                                                                                                                                                25-NOV-2004
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CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 254.2; DB 2;
Pred. No. 1e-52;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 33; 39pp; English.
                                                                                                                                                   TGCTACTTTCCTTGTTAAT 259
                                                                                                                                                                                         241 récrácitricciricair 259
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                                                                                                                                                                                                                                                                                    BP.
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98.8%;
                                                                                                                                                                                                                                                                                    AAQ70130 standard; cDNA; 288
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Watches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Powell KA,
                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial Rs-AFP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-249223/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZENE ) ZENECA LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR57327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1994.
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14-FBB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dubock AC,
                                                                                                                                                                                                                                                                                                                          AAQ70130;
                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA represents the sequence of Rs-AFP2 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage R408. Inserts from 22 positive clones were excised by EcoRI digestion and insert sizes of approx. 400bp the others between 250-300bp. The inserts of their sizes of approx. 400bp the others between 250-300bp. The inserts of the largest clones were then sequenced and found to differ only in the largest clones were then sequenced and found to differ only in the largest sequence was identified as R5-AFPI. So the R8-AFPI. So the R8-AFPI site directed mutagenesis. (Updated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                         Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cammue BPA, Osborn RW, Rees SB, Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 254.2; DB Pred. No. 1e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to correct PN field.)
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 21; Fig 35; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  91GB-00018523.
92GB-00003038.
92GB-00013526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ICIL ) IMPERIAL CHEM IND PLC.
                                                                                                                                                                                                                                                                                                                                                                92WO-GB001570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.4%;
(revised)
(first entry)
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Best Local Similarity 98.8
Matches 256; Conservative
                                                                                                                                                                                                                          16. .256
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-100978/12.
                                                                                                                                                                       Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Broekaert WF, (
Vanderleyden J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-1991;
13-FEB-1992;
25-JUN-1992;
                                                       RB-AFP2 CDNA.
                                                                                                                                                                                                                                                                                    WO9305153-A1
                                                                                                                                                                                                                                                                                                                                                                27-AUG-1992;
25-MAR-2003
07-JUL-1993
                                                                                                                                                                                                                                                                                                                          18-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
121 ccaagreceacarecreaceacrerereaaacaaraacecarecaagaareagrecarr 180
                                                                                 240
                                                                                                                        181 AGACTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial; Rs-AFP2; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; PCR; polymerase chain reaction; mutagenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
                                                                             AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
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121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
                                                                                                              AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATC 250
                                                                                                                                                                                                   TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
                                                                                                                                                                                                                        251 IGCTACTICCCAIGTTAATCTACCAAGAGCTCTTAATGCTTAATTATAAAGTGTGTATTT 310
                                                                                                                                                                                                                                                                  Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
protein expression; plant defensin; RSAFP2; antifungal protein; AFP2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
                                               GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
                                                                  Ġrażakackaracickiechkaciczieczacckiechracicitrictricechecierri
                                                                                                                                                  AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCCAGCTCACAAGTGTATC
                                                                                                                                                                                                                                                     301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT
GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "fusion protein of DmAMP1 and RsAFP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding a fusion protein of DmAMP1 and RSAFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Bolle MFC,
                                                                                                                                                                                                                                                                                                       GTTGGTTCGGTTATACAAATAAAGTTTT 388
                                                                                                                                                                                                                                                                                                                      |||| || || ||| 398
GTTGCTTTGTTTTATAGGTAAACTTT 398
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3...566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 34; 151pp; English
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98GB-00026753
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                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-246564/21.
P-PSDB; AAY84072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZENE ) ZENECA LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dahlia merckii.
Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ99339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                         267
CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
             148 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 207
                                                AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes the Arabidopsis PDF1.1 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Terras FRG, Manners JM;
                                                              Gaps
                                                                                                                                                                                                                                                                                      Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
fungi; ss.
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Best Local Similarity 76.5%; Pred. No. 9e-50;
Matches 297; Conservative 0; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/product= "PDF1.1"
/note= "plant defensin"
                                                                                                                                                                                                                                                                                                                                                         cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 1, 72pp, English.
                                                                                                 241 TGCTACTTTCCTTGTTAAT 259
                                                                                                                    268 TGCTACTTTCCTTGTTAAT 286
                                                                                                                                                                                          BP
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                                                                                                                                                                                          AAV10632 standard; DNA; 403
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26. .113
/*tag= b
114. .265
                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                  A. thaliana PDF1.1 DNA
                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
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                                                                         208
                                                181
121
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JA;

Ray

Evans IJ,

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96GB-00013753
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                                                                              WPI; 1998-086663/08.
                       5
                                                                                         P-PSDB; AAW40346.
                       (ZENE ) ZENECA
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                                             Broekaert WF,
  01-JUL-1996;
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                                                                                                                                                                                                                                                                                    Query Match
                                                         Kazan K;
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                                                                                                                                                                                                                                                                                    GCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGCCCAAGTGGG 129
                                                                                                                                                                                                                                                                                                                              ACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAG 189
                                                                                                                                                                                                                                                                                                                                                                            249
                                         improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence
                                                                                                                                                                                                                                                                                                         437
                                                                                                                                                                                                                                                                                                                                                     ACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGACTTGAG 497
                                                                                                                                                                                                                                                                                                                                                                                                AAAGCACGACATGGATCTTGCAACTATCGTTTCCCAGCTCACAAGTGTATCTGCTACTTT 557
 The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlina antimicrobial protein (AMP) 1 and the antifungal protein 2 (RsAFP2), linked by a linker propeptide of the invention. The specification describes methods for
                                                                                                                                                                                                                                        69
                                                                                                                                                                                                                                                    318 GGCCCATGGCTAAGTTTGCGTCCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTT
                                                                                                                                                                                                                                       10 GTGATCATGCCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTT
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                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                          Length 575;
                                                                                                                                                                     Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                 11;
                                                                                                                                                                                            DB 3;
                                                                                                                                                                                        Score 232.4; DB 3
Pred. No. 2.8e-47;
0; Mismatches 11
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/product= "PDF1.2"
/note= "plant defensin"
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120..271
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/*tag= a
32. .119
                                                                                                                                                                                                     Best Local Similarity 95.6
Matches 239; Conservative
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 ACGTCCCATGTTAAATCTACCACTAATCTTTGGTGCTAAATCGTGTGTATTTTACATAAA 320
                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes the Arabidopsis PDF1.2 gene which is used in a novel method for the protection of plants against pathogens which involves inducting expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
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Manners JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 TTGAAGGAGCCAAACATGGATCATGCAACTATGTCTTCCCAGCACACAGTGTATCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S TATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 TAATAATCATCATCGCTAAGTTTGCTTCCATCATCACCCTTATCTTCGCTGCTCTTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 retringerectrinegaegeaccaccaangeregaageacacaaaagrierecaagaagecaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 TITITIGCIGCITICGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAA
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7
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Penninckx IAMA, Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 AATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTA 347
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                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 72pp; English.
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   врнл,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 79.9
Matches 274; Conservative
                                                                                                                                                                                                                                                                         gene from Arabidopsis.
Thomma
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WPI; 2002-055861/07. 27-DEC-2001

Cooper Wang X, Han B, Zhu T, (SYGN) SYNGENTA PARTICIPATIONS AG Chang H, 22-JUN-2001; 2001WO-IB001104. 2000US-0213848P. 2000US-0214087P. 2000US-0258692P. Budworth P, Brown D, 23-JUN-2000; 23-JUN-2000; 29-DEC-2000;

Promoters for root-specific, leaf-specific or constitutive regulation of plant gene expression, useful for regulating the expression of selected transgenes (e.g. stress tolerance and defence related genes) in economically important plants.

Disclosure; SEQ ID NO 607; 290pp; English

The invention relates to promoters for root-specific, leaf-specific or constitutive regulation of plant gene expression. Also included are an isolated polymucleotide (NI) (comprising a plant nucleotide sequence that directs root-specific transcription of an operatively linked nucleic acid sequence that directs root-specific transcription of an operatively linked nucleic acid sequence is from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by an Arabidopsis gene comprising a promoter selected from the polypeptide encoded by an Rice gene comprising a promoter selected from polypeptide encoded by an Rice gene comprising a promoter selected from the polypeptide encoded by an Rice gene comprising a promoter selected from Doperatively linked nucleic acid segment in a plant cell, where the plant nucleotide sequence is from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by an Arabidopsis gene comprising a promoter selected from ADZ745326 and ADZ73506, ADZ75006, ADZ7501, ADZ7503-ADZ7506, ADZ7501, ADZ7503-ADZ7506, ADZ7501, ADZ7503-ADZ7484-ADZ74830, ADZ786-ADZ75006, ADZ7501, introducing the expression cassette. for the expression cassette, the open reading frame is from an insect resistance gene, a bacterial disease resistance gene, a viral disease resistance gene, a viral disease resistance gene, a unal disease resistance gene, a nematode disease resistance gene, a herbicide composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a gene affecting plant agronomic characteristics, or an environment or stress resistance gene. The stress resistance gene confers resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, excessive salet, or excessive oxidative stress. The promoters are useful for regulating the expression of selected transgenes in economically important plants. For expression of selected transgenes in economically important plants. For example, root-specific promoters may be useful for expressing defenseralted genes, including those conferring insecticidal resistance and stress tolerance genes, e.g., salt, cold or drought tolerance, and genes for altering nutrient uptake, and leaf-specific promoters may be useful for producing large quantities of protein, for expressing oils or

proteins of interest, and genes for increasing the nutritional value of a plant. Constitutive promoters are useful for expressing a wide variety of genes including those which alter metabolic pathways, confer disease resistance, for protein production, e.g., antibody production, or to improve nutrient uptake. The present sequence is an open reading frame from an Arabidopsis leaf specific promoter gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 244 245 ACTITICCTIGITIAATTTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTTACACAA 304 81 retrinscriscririca Accaeca Aranga a de a constanta de accepta de a constanta d 184 201 Trigaaggagccaaacarggarcargcaacrargrerreceagcacacaagrerrerer 260 261 ACGICCCATGITAAAICTACCACTAAICTITGGIGCIAAAICGIGIGIATITITACATAAA 320 64 5 TATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTC 21 raaraarcarcacaraacrirecriccarcarcaccriarcricecrecristri GTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACC TTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCT TTTTTGCTGCTTTCGAAGCACCACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAA Gaps 5 53.9%; Score 223; DB 7; Length 400; 79.9%; Pred. No. 5.2e-45; lidels 305 AATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTA 347 Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other; 321 AATAAGTCNCTGTCAC--TCTNTGAGTAACTTTATGACATGCA 361 Best Local Similarity 79.9 Matches 274; Conservative 125 65 185 Query Match 88888888888888 셤 g 유 셤 g ઠે à ਨੇ à

Search completed: May 10, 2006, 02:39:16 Job time : 673 secs

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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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/note="vector: pDNR-LIB CREATOR; Site_1: SfiIA; Site_2:
/sfilb; Sequences have been trimmed to_remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."
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Contact: Ed Tsang
Plant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatcoon, 2510 May, Canada
Tel: 306 975 4164
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High quality sequence stop: 484
Location/Qualifiers
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Eudicotyledons; Core eudicotyledons; rosida; eurosida II; Brassicales; Brassicacea; Brassica.

1 (bases 1 to 566)

2 Fei,H., Li,F., Tsang,E. and Cutler,A.
Gene expression in germinating and dormant seeds of Brassica napus
L Unpublished (2004)

2 Contact: Adrian Cutler
Signaling and Plant Metabolism
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 5891
Fax: 306 975 4839

Email: Adrian.Cutler@nrc-cnrc.gc.ca
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Brassica napus 3ETMS Brassica napus
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 547)
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                                                                111 GTTCTTTTCGCTGCTTTCGAAGCACCACAATGGTGGAAGCACAGAAGTTGTGCGAGAGG 170
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(www.tigr.org)."
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/do xref="taxon:3708"
/db xref="taxon:3708"
/clone lib="Brassica napus 3ETMS"
/note="Vector: pDNR-LIB_CREATOR; Site_1: SfilA; Site_2: SfilB; Sequences have been trimmed to remove vector and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTTTATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTT
                                                                                                                                                                                                                                                                                     National Research Council of Canada Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, Saskatchewan, S7N 0W9, Canada Tel: 306 975 4164 Fax: 306 975 4839 Email: Ed.Tsang@nrc-cnrc.gc.ca High quality sequence stop: 547.
                                                                                                                                           CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
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Contact: Ed Tsang
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/organism="Brassica napus"
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CDNA 5', mRNA sequence.
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Brassica napus
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/mol_type="mRNA"
/mol_type="mRNA"
/clone_lib="staxon:3708"
/clone_lib="staxon:3708"
/note="Vector: pDNR-LIB_CREATOR; Site_1: SfilB, Site_2: SfilB; Sequences have been trimmed to remove vector and low quality regions using LUCY sequence cleanup software (www.tigr.org)."
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Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
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Contact: Ed Tsang
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Pred. No. 6.3e-69;
0; Mismatches 41
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High quality sequence stop: 485.
Location/Qualifiers
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llarity 89.4%;
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38TMS UP 002 All 10JUN2003_048 Brassica napus 3RTMS Brassica napus
CDNA 5', mRNA sequence.
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                                      169 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCGTTT 228
                                                                                                            229 AACCTTGAGAAAGCACGACATGATCTTGCAACTATGTCTTCCCAGCTCACAAGTATT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                                                301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
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//mol_type="mRNA"
/db_xref="texxon:3708"
/clone lib="Brassica napus 3ETMS"
/note="Vector: pDNR-LIB_CREATOR; Site_1: SfilA; Site_2:
SfilB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."
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                                                                                        AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC
                                                                                                                                                                                                                                                                                                      Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Fax: 306 975 4839
High quality sequence stop: 484.
Location/Qualifiers
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0; Mismatches 41
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National Research Council of Canada
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Unpublished (2004)
Contact: Ed Tsang
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Brassica napus
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Best Local Similarity
Matches 372; Conserv
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CN726272
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181 ANCCTTGGGAAACCACGACGACGACGACGACGACCACCACCACCAC		241 TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300		351 ATAAAATAAGTCTGTGTCACTACCAATGAGTGATTTTATGACATGTACCTGATATATGTT 410	359 ATGTTGGTTGGTTATACAAATAAAGTTTTATTCACCAAAAAAAA	411 ATGTTGGTTATA-ATAAAAGTTTTATGCGCAAAAAAAAAA	661 661	CN726661 4.56 DP MKNA 11REAT EST 14-FMAI-200 N 3ETMS UP 006 G02 10JUN2003 002 Brassica napus 3ETMS Brassica napus control 27, mRNA sequence.	N N SO	NISM		Gen	JUDKNAL Unpublished (2004) COMMENT Context of Fang	Plant Natural Producti of Canada National Research Council of Canada Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,	Saskatchewan, S7N OW9, Canada Tel: 316 975 4164	rax: suo s/s 4059 Email: Ed.Teang@nrc-cnrc.gc.ca Hich mislity semience afon: 456		/organism="Brassica napus" /mol_type="mRNA"	/db_xref="taxon:3708" /clone lib="Brassica napus 3ETMS" /acton="totops" repared strain	Indice vector: punk lie transcription of still streets Sfills. Sequences have been trimmed to remove vector and low muslity regions using LUCY sequence cleanup software	(www.tigr.org)."	77.3%; Score 320; DB 7; Length 456; nilarity 87.9%; Pred. No. 7.5e-68;	Matches 364; Conservative 0; Mismatches 40; Indels 10; Gaps 1;	1 GITTIAITAGIGAICAIGGCIAAGIITGCGICCAICAICACCACTICITITIGCGICICIT 60		GITCITITIGCIGCITITCGAAGCACCAACAAIGGIGGAAGCACAGAAGITGIGCGAAAGG	GTCCTTTTCGCTGCTCTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAGAGG	121 CCAAGTGGGACATCACAGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180	AACCTTGAGAAAGCACGACATGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 24	216 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATT 275
191 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAACAACAACAACAACAACAACAACAACAACAACAA	qa	රු දි	ò	QQ	ò	đ	RESULT CN7266	DEF:	ACCI VERS	rios O	REFE	A	COM				FEA				ORIGIN	Бă	Ĭ	ò	q	ò	q	ò 1	B ò	7 A
QY Q	STATC	STATT		ACAAAATAAGTCAGTGACACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTT		ATGTTGGTTCGGTTATACAAATAAAGTTTTATTCACCAAAAAAAA	*** AIGIIGGIIRIR-AIMMANGIIIIRIGGACCALCANAMANAMANAMANAMANAMANAMANAMANAMANAMANA	CN726255 481 bp mRNA linear EST	SETMS CDNA C	CN726255.1 S EST.	SM			Unpublished (2004) Contact: Ed Tsang Plant Natural Products	nada 110 Gymnasium Place, Saska	Saskatchewan, S/N UW9, Canada T= 1306 975 4164 F==: 306 975 409	Fax: 300 9/3 4839 Email: Ed. Rangenro-cnro.go.ca High quality sequence stop: 481.	н г	/organism="Brassica napus" //organism="Brassica napus" //organism="Brassica napus"	/db xret="taxon:3/08" /clone lib="Brasica napus 3ETMS" //orb="Wortor" namus ITS TREATOR. Sits 1. Séits. Sits 2.	Sfiles Sequences have been trimmed to remove vector and stiles. Sequences have been trimmed to remove vector and low quality regions using LUCY sequence cleanup software (time time to)	ORIGIN (****-LIGI.OIG).	tch 78.0%; Score 322.8; DB 7; Length al Similarity 89.2%; Pred. No. 1.5e-68;	371; Conservative 0; Mismatches 42; Indels 3; Gaps	CTCTT	giattactactecececeaectrectrecateatrecececectrifice	GTTCTTTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAAAAGGAAGG	GTTCTTTTCGCTGCTTTCGAAGCACCAATGGTGGAAGCACAGAAGTTGTGCGAGAGG	CCANCING CANCING CONTROLL CONTROLL CANCING CONTROLL CANCI	AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC

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CN726329 597 bp mRNA linear EST 14-MAY-2005
3ETMS UP 002 G01 10JUN2003_002 Brassica napus 3ETMS Brassica napus
CDNA E', mRNA sequence.
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                                                          360
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                                                                                             395
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1. .597
/organism="Brassica napus"
/organism="Brassica napus"
/mol_type="mkNa"
/db xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/clone_lib="wector"
/clone_lib="guence have been trimmed to_remove vector and low quality regions using LUCY sequence cleanup software (www.tigr.org)."
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                                                                                     336 ATAAAATAAGTCTGTGTCACTATCAATGAGTGATTTTATGACATGTACCTGATATGTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, Saskatchewan, S7N 0W9, Canada Tel: 306 975 4164 Fax: 306 975 4839
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Contact: Rd Taang
Plant Natural Products
National Research Council of Canada
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High quality sequence stop: 597
Location/Qualifiers
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88.6%;
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3BTMS UP_007_B11_11JUN2003_047 Brassica napus 3BTMS Brassica napus
cDNA 5', mRNA sequence.
CN726701 GI:65284503
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                                                            276 rGCTACTTCCCTTGTTAACTTATGCGCAAACTCTTTGGTGGTTAGTTTTGGTAATTTAC 335
                                                                                                 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
                                                                                                                                        336 ATAAAATAAGTCTGTGTCACTATCAATGAGTGATTTTTATGACATGTACCTGATATGTTAT 395
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/note="vector: pDNR-LIB CREATOR; Site_1: SfilA; Site_2:
SfilB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."
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                        TGCTACTTTCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC
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Contact: Ed Tsang
Contact: Ed Tsang
Hant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Sa Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Pax: 306 975 4839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 316.4; DB 7;
Pred. No. 5.7e-67;
0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .458
/organism="Brassica napus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Ed Teangenre-cnrc.gc.ca
High quality sequence stop: 458.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
76.4%;
Best Local Similarity 85.3%;
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica napus (rape)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 458)
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CN726701
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DEFINITION
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VERSION
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Eukaryota, mayua;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
Tosids; eurosids II; Brassicales; Brassicaceae; Brassica.
Sharpe, A.G., Gjetvaj, B., Durkin, J. and Lydiate, D.J.
Brassica napus ESTS
AL Uppublished (2004)
Contact: Sharpe, A.G.
Molecular Genetics
Agriculture & Agri-Food Canada
107 Science Place, Saskatoon, Sakatchewan, Canada, S7NOX2
Tel: 306 956 7271
Ext. 306 956 7277
                                                                                                                                                                                               CNB26227

SLI386 Brassica embryo library (EL) Brassica napus cDNA clone ELI386 complete, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
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336 ATAAAATAAGTCTGTGTCACTATCAATGAGTGATTTTATGACATGTACCTGATATGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GIICITITITGCIGCITICGAAGCACCAAAAATGGIGGAAGCACAGAAGITGIGGGAAAGG
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                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: sharpea@agr.gc.ca
Seg primer: M13 Forward and T7.
Location/Qualifiers
                                                                                                                                                                                                                                                                    CN826227
CN826227.1 GI:65296011
                                                                                                                                                                                                                                                                                                                               Brassica napus (rape)
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CN826227
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KEYWORDS
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                                                                                                                                                                                                                                             CN726424 453 bp mRNA linear EST 14-MAY-2005 TENW UP 003 H02 10JUN2003_001 Brassica napus 3ETMS Brassica napus CDNA 5', mRNA sequence.

CN726424
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bopermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATT 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Brassica napus"
/mol_type="mRAM"
/mol_type="mRAM"
/db_xref="t-axon:3708"
/clone_lib="Brassica napus 3ETMS"
/clone_lib="Brassica napus 3ETMS"
/note="weetcr: pDNR-LIB YERATOR'S; Site_1: SfilA; Site_2:
SfilB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene expression in seed germination in Brassica napus Unpublished (2004)
Contact: Ed Tasang
Plant Natural Products
National Research Council of Canada
Plant Blotechnology Institute, 110 Gymnasium Place, Saskatoon, 538 Katchewan, 57N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.1%; Score 315.2; DB 7; Length 453; 87.2%; Pred. No. 1.1e-66; ive 0; Mismatches 43; Indels 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Ed.Teangenrc-cnrc.gc.ca
High quality sequence stop: 453.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (www.tigr.org)."
                                                                                                                                                                                                                                                                                                              CN726424.1 GI:65284226
EST.
                                                                                                                                                                                                                                                                                                                                                                     Brassica napus (rape)
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Best Local Similarity
Matches 361; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsang, E.
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CD831680
BN40.060H13F011227 BN40 Brassica napus cDNA clone BN40060H13, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                               Brassica napus (rape)
Brassica napus
Brassica napus
Brassica, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosida II, Brassicales, Brassicaceae; Brassica.
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 231 AACCTIGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCCAGCTCACAGTGTATT 290
                                                                     291 TGCTACTTCCCTTGTTAACTTTATGCGCAAACTCTTTGGTGGTTAGTTTTGTGTAATTTAC 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93, the Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoplante, a major partnership french program in plant genomics (pubblished (2003)
Contact: Genoplante Genoplante Genoplante
                                   TGCTACTTTCCTTGTTAATTTTATCGCAAACTCTTTGGTGAATAGTTTTTTATGTAATTTAC
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                                                                                                        ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTTAAGACATGTACC--AGATATGTT
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                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 311.2; DB 6;
Pred. No. 1.1e-65;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .470
/organism="Brassica napus"
/mol type="mRNA"
/cultivar="Jet Neuf"
/db xref="taxon:3708"
/clone="RNA0060H13"
/tissue type="seed"
/clone_lib="BNA0"
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TITLE
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CD831680
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                                                                                                                                                                                                                                                                                                                                                     458 bp mRNA linear BST 10-JUL-2003
BN45.043006F011229 BN45 Brassica napus cDNA clone BN45043006, mRNA
Sequence.
CD834994
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                                                    193 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATT 252
                                                                                                                             51 GTATTACTAGTGAGGATGGCTAAGTTTGCTTCCATCATTGCCCCACTTTTTGCTGCTCTT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATC 240
CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 192
                                                                                                       TGCTACTITCCTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTAC 300
                                                                                                                                                                            ACAAAATAAGTCAGTGTCACTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
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This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Pred. No. 2.5e-66;
0; Mismatches 43
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/cultivar="Jet Neuf"
/db_xxef="teaxon:3708"
/clone="BN45043006"
/tissue_type="seed"
/clone_lib="BN45"
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Best Local Similarity 88.7%;
Matches 362; Conservative
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Brassica napus (rape)
Brassica napus
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CDB32071 452 bp mRNA linear EST 10-JUL-2003
BN40.061003F011227 BN40 Brassica napus CDNA clone BN40061003, mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 IGCIACITICCITGITAAITITAICGCAAACICITIGGIGAATAGITITIAIGIAAITIAC 300
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351 ATAAAATAAGTCTGTGTCACTATCAATGAGTGATTTTATGACATGTACCTGATATATGTT 410
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This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
Location/Qualifiers
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Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GTTCTTTTTGCTGCTTTTCGAAGCACCAAAATGGTGGAAGCACAGAAGTTGTGCGAAAGG
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Pred. No. 1.2e-65;
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/mol type="mRNA"
/cultivat="Jet Neuf"
/db_xref="taxon:3708"
/clone="RNA"
/tissue type="seed"
/clone_lib="BN40"
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                                                      359 ATGTTGGTTCGGTTATACAATAAAGTTT
                                                                                   411 ATGTTGGTTCGGTTATAAAAAGTTTT
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Matches 347; Conservative
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                                                                                     ATAAAATAAGTCTGTGTCACTATCAATGAGTGATTTTATGACATGTACCTGATATATGTT 432
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     TGCTACTTCCCTTGTTAACTTATGCGCAAACTCTTTGGTGGTTAGTTTTGTGTAATTTAC 372
                                                      ACAAAATAAGTCAGTGCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93, rue Henri Rochefort 91025 EVRY CEDEX France
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Flats sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Pred. No. 1.2e-65;
0; Mismatches 40;
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Matches 347; Conservative
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415 ATGTTGGTTCGGTTATAATAAAAGTTTT 443

Search completed: May 10, 2006, 06:32:17 Job time : 3758 secs

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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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U18557 Raphanus and A26875 R. sativus A A33404 Sequence 19 AR050153 Sequence 123728 Sequence 48 AR30272 Sequence 48 AR374914 Sequence AR642703 Sequence AR642709 Pappanus a B0174927 Disease t B31545 Ancibacteri AB012871 Wasabia j U59459 Brassica na X97318 R. sativus m
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AX50251 Sequence
AX590057 Sequence
AX133787 Arabidops
A86847 Sequence
BD174928 Disease t
AF528180 Brassica
AF528180 Brassica
AR528160 Sequence
AX412406 Sequence
AX412406 Sequence
AX412406 Sequence
AX412406 Sequence
AX412601 Sequence
AX651878 Sequence
AX651878 Sequence
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1 (bases 1 to 285)
Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
fungi
Patent: US 5773696-A 17 30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 05-DEC-1998
      AR130280 Sequence
123736 Sequence 58
AR014692 Sequence
AR432392 Sequence
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X91916 A.thaliana
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AY060506
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AR432392

AR432392

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A39649

A63964

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AR20733

AR374914

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BD13428

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BB1545

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AX412406
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AR014693
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AR432393 Sequence
A39553 Sequence 41
                                                                May 10, 2006, 05:46:44 ; Search time 3626 Seconds (without alignments) 1881.195 Million cell updates/sec
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        GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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AR432393
A39553
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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Maximum DB seq length: 2000000000
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PAT 29-SEP-1999
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                                                           1 (bases 1 to 288)
Dubock,A.C., Powell,K.A. and Rees,S.B.
ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
PATENT: WO 9416076-A 41 21-JUL-1994;
ZENECA LID (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 288)
Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 5824869-A 58 20-OCT-1998;
Location/Qualifiers
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Location/Qualifiers
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Sequence 58 from patent US 5824869.
AR050161.1 GI:5972153
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unidentified
unclassified sequences.
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                                                                                                 21 PheGlualaProThrMetValGlualaGlnLysLeuCysGlnArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                             Unknown.
Unclassified.
1 (bases 1 to 285)
Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 17 25-NOV-2003;
Monsanto Technology LLC; St. Louis, MO
Locatorology LLC; St. Louis, MO
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Sequence 17 from patent US 6653280.
AR432393
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Sequence 41 from Patent WO9416076.
A39553
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                          US-09-759-584-59 (1-80) x AR014693 (1-285)
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and Rosenberger, C. Annette. controlling plant pathogenic
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                                    Rees, S.B.,
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                                   Cammue, B.P.A., Osborn, R.W.,
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Liang, J., Shah, D.Maganlal., Wu, Y.Shun. Antifungal polypeptide and methods for fungi.

Patent: US 5773696-A 16 30-JUN-1998;
Location/Qualifiers
          Unclassified.

1 (bases 1 to 288)

1 Stocksert, W.F., Cammue, B.P.A., Osborn, J. Terras, F.R.G. and Vanderleyden, J. Biocidal proteins
Patent: US 5538525-A 58 23-JUL-1996;
Location/Qualifiers
1. .288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16 from patent US 5773696.
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                                                                                 103 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCCAAAGGCCAAGTGGGACATGG 162
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                       21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp
                                                                 21 PheGluhlaProThrMetValGluhlaGlnLysLeuCysGlnArgProSerGlyThrTrp
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Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 6187704-A 58 13-FEB-2001;
Location/Qualifiers
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Sequence 58 from patent US 5538525.
123736
123736.1 GI:1603606
                                                                                                                                                                                                                                 AR130280 288 bp 1
Sequence 58 from patent US 6187904.
AR130280.1 GI:14118177

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US-09-759-584-59 (1-80) x AR050161 (1-288)
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RESULT 5 AR130280 LOCUS DEFINITION

PAT 05-DEC-1998

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/brotein id="AAA69541.1"
/db_xref="G1:609322"
/translation="MAKPASIIALLFAALVLFPAFEAPTMVEAQKLCERPSGTWSGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="antifungal protein 1"
/function="antifungal, fungistatic"
/function="antifungal, fungistatic"
/funct="Rayidence for antifungal activity: Analysis of two
novel classes of antifungal proteins from radish (Raphanus
sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
                 1 (sites)
Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,
Osborn,R.W., Kester,A., Rees,S.B., Torrekens,S., Van Leuven,F.,
Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.
Small cysteine-rich antifungal proteins from radish: their role in
host defense
                                                                                                                                                                             Direct Submission
Submitted (14-DBC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
On Peb 9, 1995 this sequence version replaced gi:609321.
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cosids; eurosids II; Brassicales; Brassicaceae; Raphanus
                                                                                                                                                                                                                                                                                                            /organism="Raphanus sativus"
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1.395
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/note="18 A nucleotides"
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Chem. 267, 15301-15309"
/citation=[1]
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Plant Cell 7, 568-573 (1995)
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/gene="R8-AFP1"
102. .254
/gene="R8-AFP1"
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395 bp mRNA linear PLN 07-JUL-1995 sephanus sativus antifungal protein 1 preprotein (Rs-AFP1) mRNA, complete cds.
U18557
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Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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                 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp
                                                                                         41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla
                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.

I (bases I to 285)

Ling,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.

Antifung,J., Shah,Deptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi

Patent: US 653280-A 16 25-NOV-2003;

Monsanto Technology Lic; St. Louis, MO

Location/Qualifiers
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Sequence 16 from patent US 6653280.
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PATENT: WO 9721814-A 19 19-JUN-1997;
ZENECA LTD (GB)
Other publication AU 1105397 19970703.
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Sequence 19 from Patent W09721814.
A63404
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unclassified sequences.
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Raphanus sativus
Raphanus sativus
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
I (bases I to 414)
Brochkaert, W.F., Cammue, B.P.A., Terras, F.R.G., Vanderleyden, J.,
Osborn, R.W. and Rees, S.B.
PalOCIDAL PROTEINS
Patent: WO 9305153-A 33 18-MAR-1993;
ICI PLC (GB)
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unclassified sequences.

1 (bases 1 to 414)

1 (bases 1 to 414)

Author, A.C., Powell, K.A. and Rees, S.B.

ANTIMICROBIAL-PROPEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
PATENT: WO 9416076-A 37 21-JUL-1994;

ZENECA LTD (GB)

Other publication AU 5820494 940815.

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Mismatches:
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Sequence 37 from Patent W09416076.
A39549
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R.sativus AFP1 gene.
A26875
A26875.1 GI:1247352
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61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCys1leCysTyrPheProCys 80
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Unknown.
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Unclassified.
I (bases 1 to 414)
Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 5538525-A 48 23-JUL-1996;
Location/Qualifiers
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Sequence 48 from patent US 5538525.
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123728.1 GI:1603598
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1 (bases 1 to 414)
Broskaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Blocidal proteins
Patent: US 6187904-A 48 13-FEB-2001;
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Sequence 48 from patent US 6187904.
AR130272.1 GI:14118169
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Search completed: May 10, 2006, 08:02:43 Job time : 3630 secs

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Aat72333 |
Aat68696 |
Aaa53190 |
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07-JUL-1993
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  AAQ38652;
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  Aaq38652 Rs-AFP2 c
Aaq70130 Antimicro
Aaq38650 Rs-AFP1 c
Aaq70128 Antimicro
                                                                                                                                 May 10, 2006, 05:44:15 ; Search time 452 Seconds (without alignments) 1769.387 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                1 MAKFASIIALLFAALVLFAA......RHGSCNYVFPAHKCICYFPC
                    GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9993994
                                                                                              OM protein - nucleic search, using frame_plus_p2n model
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Match Length
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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Оатараве :

441 441 433 433

Result No.

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Plant-derived antimicrobial proteins are expressed in endosymbiotic clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPI from R. sativus. The full-length CDNA sequence of PCR assisted site-directed mutagenesis of Rs-AFP2 is given in AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-MAR-2003 to correct PN field.)
                                             Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte;
PCR; polymerase chain reaction; mutagenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 33; 39pp; English
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                  Antimicrobial Rs-AFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-249223/30.
                                                                                                                                                                                                                                                                                                                                          (ZENE ) ZENECA LTD.
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                                                                                                                                         Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR57327
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                                                                                                                                                                                                                                                                                                               This cDNA represents the sequence of Rs-APP2 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino caids 2 to 7 of Rs-APP1 and has a sense crientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and igoxigenin-11-dTPP instead of dTPP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript pagemid form with the aid of helper phage the chers between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in the 1 largest clones were then sequenced and found to differ only in the langth of their 5' and 3' UTR's. The longest sequence was identified as Rs-APP1 so the Rs-APP2 was seen to differ by only 2 amino acids from nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
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                                                                                                                                                                                                   Biocidal proteins isolated from seeds of plants - e.g. brassica or
dahlia, useful for increasing plants' resistance to fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCCAAAGGCCAAGTGGGACATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
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                                                                                                 Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                   Rees SB,
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                                                                                                   Osborn RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-759-584-59 (1-80) x AAQ38652 (1-261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                Example 21; Fig 35; 110pp; English.
                                                          (ICIL ) IMPERIAL CHEM IND PLC
  92GB-00003038.
92GB-00013526.
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                                                                                                   Cammue BPA,
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Best Local Similarity:
                                                                                                                        Vanderleyden J;
                                                                                                   Broekaert WF,
  13-FEB-1992;
25-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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14-FEB-1995
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Query Match

ઠ 셤 ò 요 ò 셤 ઠે 셤 RESULT 2

SXEE

162

102 40

288 00000 0000

222

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282

80

18-MAR-1993

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Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
    76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-APPI from R. sativus. The full-length cDNA sequence of Rs-APPI is given in AAQ70128. (Updated on 25-MAR-2003 to
                                                                                                                                                   196 CGACATGGATCTTGCAACTATGTTTCCCAGCTCACAAGTGTATATTTCTTCTTGT
                                                                                                                             61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                              41 SerGlyvalCygGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ATGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 31; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SB;
                                                                                                                                                                                                                                                        AAQ70128 standard; cDNA; 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-GB000012.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.55e-43
433.00
98.8%
97.5%
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial Rs-AFP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-249223/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR57325.
                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9416076-A1
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                                                                                                                                                                                                                                                                                                  AAQ70128;
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                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA represents the sequence of Rs-APP1 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA 11bray. This primer corresponds to amino acids 2 to 7 of Rs-APP1 and has a sense crientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and ingoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage (2 their size compared by agarcse gel electrophoresis. Four clones had insert sizes of approx. 400bp the others between 250-300bp. The inserts of the largest clones were then sequenced and found to differ only in the length of their 5, and 3, UTR's. The longest sequence is given here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTTGCTGCT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetalalysPhealaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                 Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-759-584-59 (1-80) x AAQ38650 (1-414)
                                                                                                                                                                                                          Location/Qualifiers
16. .256
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 21; Fig 35; 110pp; English.
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92GB-00013526.
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433.00
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-100978/12.
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Best Local Similarity:
                                                                                                                                                                  Raphanus sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vanderleyden J;
                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-1991;
13-FEB-1992;
25-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Broekaert WF,
07-JUL-1993
                                         R8-APP1 CDNA
                                                                                                                                                                                                                                                                                                WO9305153-A1
                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-1992;
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PheGlualaProThrMetValGlualaGlnLyBLeuCygGlnArgProSerGlyThrTrp 40

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Query Match: DB:

PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp

75 40

20 75 40

414 1 1 4 1 4 0 0 0

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76 TTCGAAGACACAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGAGTGGGACATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                16 ATGGCTAAGTTTGCGTCCATCATCATCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                         41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla
                                                                                                                                                                                                                                                                                                                                           21 PheGlualaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp
                                                                                                                                                                                                                                                          1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                       Conservative:
Mismatches:
Indels:
                                                                Length:
Matches:
                                                                                                                                                                        Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT68696 standard; cDNA; 414 BP
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                                                                1.55e-43
433.00
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103. .255
/*tag= c
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P-PSDB; AAW19617.
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                                                                                                          Percent Similarity:
Best Local Similarity:
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                                            Alignment Scores:
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DB:
                                                                . No. .
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AAT68696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
  This cDNA sequence encodes an Rhapanus sativus (radish) antifungal protein, Rs-AFP12.
AAM19231, have also been produced (see AAM19282-92, AAM19294-98, AAM193301-04, AAM19330-34 and AAW11765-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease rolasistance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct plaids.)
                                                                                                                                                                                                                                                                                                                                                                                                         Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sijtsma L, Van Amerongen A;
Borremans FAM, Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16. .258
/*tags a
/transl except= (pos:85. .87, aa:Glu)
16. .102_
                                                                                                                                                                                                                                                                                                                                                                    Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product= "antifungal_protein_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Puijk WC, Schaaper WMM,
, Samblanx GW, Fant F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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(first entry)
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103. .255
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P-PSDB; AAW19280.
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28-MAR-1996;
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Broekaert W,
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19-JAN-1998
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ILD AAT72333

ILD AAT72333

AAC AAT7

AAT7

AAT7

AAT72333

BE Rapl P-19-C

SE RAPL RAPL

SE RAPL

SE
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New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
                                                       Rs-AFP1; radish antifungal protein 1; fungicide; salt tolerance; preservative; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                                          /*tag= a
/transl except= (pos:85. .87, aa:Glu)
16. .102
Radish antifungal protein 1 (Rs-AFP1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rees SB;
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rice blast disease against pathogenic microbes

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This cDNA clone codes for the preprotein for radish antifungal protein 1 (RSA-FRP1) (ARAN1961). Novel antifungal proteins are based on RSA-FRP1, Rs-AFP2 (see AAW19616), Rs-AFP3 and Rs-AFP4, especially those in which Gly9 is repaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW36371-90) of Rs-AFP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly when expressed in plants
                                                                                                                                                                                                                                                                                                                                                             Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                   40
                                                                                                                                                                                                                                                                                                                                                                                                       SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and
                                                                                                                                                                                                                                                                                                                                              PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                       MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
pathogenic microbe; radish; rice blast disease; ds.
                                                                                                               Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
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1 1 2 8 0 0 0 0
                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98JP-00288472
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                                                                                                                                                         1.55e-43
433.00
98.8%
97.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA53190 standard; DNA; 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TOYA-) TOYAMA KEN.
                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-1998;
                                                                                                                                           Alignment Scores:
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                                                                                                                                                            Pred. No.:
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protein expression; plant defensin; RBAFP2; antifungal protein; AFP2; ss.
                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
                                                                                                                                                                    PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp
                                                                                                                                                                                               SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla
                                                                                                                                                                                                                 161 TCAGGAGTCTGTGGAAATAATAACGCATGCAAGAATCAGTGCATTCGACTTGAGAAAGCA
                                                                                                                  1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
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3. .56
A. .56
/product a /product = "fusion protein of DmAMP1 and RSAFP2"
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0 Other;
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                                                                                                                                                                                                                                                                                                                                                         DNA encoding a fusion protein of DMAMP1 and RSAFP2.
                          Length:
Matches:
Conservative:
Mismatches:
94 G; 151 T; 0 U;
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                                                                            Gaps:
                                                                                               US-09-759-584-59 (1-80) x AAA53190 (1-449)
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98GB-00026753
                          3.04e-43
431.00
98.8%
96.2%
97.7%
Sequence 449 BP; 126 A; 78
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P-PSDB; AAY84072.
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                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                   Dahlia merckii.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200011175-A1
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                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH

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The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensing, the Dahlia antimicrobial protein (AMP) I and the antifungal protein 2 (RaAFP2), linked by a linker propertied of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprisaing a cleavage site, whereby the expressed polyprotein is post-translationally processed into the component protein molecules. The propertied sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence
            88888888888888888
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Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;

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383
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                                                                                                                                                              TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCCAAAAGGCCAAGTCGTACATGG
                                                                                                                                                                                                                                   ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                         SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla
                                                                                                                                                                                                              rcaggagrergradaacaaraacgeargeaagaarcagracarragacrrgagaaagea
                                                                                                                                                                                                                                            MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Brassica oleracea defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                    antimicrobial protein; defensin; transgenic plant; composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
          575
78
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        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                  (1-575)
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1. 243
/*tag= a
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          1.73e-42
426.00
97.5%
97.5%
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                                          Best Local Similarity:
                               Percent Similarity:
Alignment Scores:
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18-SEP-2001; 2001JP-00283117. 18-SEP-2001; 2001JP-00283117

JP2003088379-A

25-MAR-2003

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ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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                                                                           Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAGAGGCCAAGTGGGACATGG 120
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                                                                                                                                                         The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as disease, and leaf blight, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerGlyValCysGlyAsnAsnAsnAlaCyslysAsnGlnCysIleArgLeuGluLysAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            defensin.
                                                                                                                                                                                                                                                                                                        Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                      Claim 3; SEQ ID NO 1; 34pp; Japanese.
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423.00
96.2%
95.0%
95.9%
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                                    WPI; 2003-621123/59.
P-PSDB; ADC51222.
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Best Local Similarity:
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DB:
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Example

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Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgHisGlySerCysAsnTyzValPheProAlaHisLysCysIleCysTyrPheProCys 80
                                                                                                                                                                                                                                                                                                                The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein acquences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 3; 34pp; Japanese.
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                                                                          18-SEP-2001; 2001JP-00283117.
                                     18-SEP-2001; 2001JP-00283117.
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416.00
95.0%
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/*tag=
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P-PSDB; ADC51224.
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Best Local Similarity:
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 25-MAR-2003.
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DB:
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                                                                                                                                                                    antimicrobial activity, useful
                                                                                                                                                                                                                                                             The invention comprises the amino acid and coding sequence of an antimicrobial protein obtained from Brassica sp. The DNA and protein sequences of the invention are useful in the production of a multiple disease resistant plant. The present cDNA sequence encodes the Brassica oleracea defensin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGGCTAAGTTTGTGTCCATCATTGCCCTACTTTTTGCTGCTCTTGTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CGACATGGATCTTGCCAAGCTCCCAGCTCACAAGTGTATTTGCTACTTCCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antimicrobial protein; defensin; transgenic plant; composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "Втаввіса defensin protein"
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1 1 0 0 0
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Mismatches:
Indels:
                                                                        (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                   Novel Brassica sp. derived protein having antimi
for producing multiple disease resistant plants
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Matches:
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                                                                                                                                                                                                                           2; SEQ ID NO 1; 16pp; Japanese.
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07-JUN-2004; 2004JP-00168986
                                   18-SEP-2001; 2001JP-00283117
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423.00
96.2%
95.0%
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/*tag=
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P-PSDB; ADU71301.
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Best Local Similarity:
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41

Query Match: DB:

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ADC5122 RESULT

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XPXTTFXSXTTFXSXTTFXSX

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The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Eutrema wasabi (Wasabia japonica) gamma-thionin protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 rcaggagrereregaaacaacaaregegegegagaarearegegereearegagagagaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:1.
                                                                                                                                                                                             A disease-resistant plant in which wasabi gamma-thionin gene introduced, creation of the disease-resistant plant.
                                                                                                                                                                                                                                                                                                                                                                               55 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wasabia japonica antibacterial protein encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                           243
0 4 0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wasabia japonica; antibacterial; food additive; ds
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/product= "antibacterial protein"
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                            Claim 3; Page 8; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                 60 A; 54 C;
                                                       22-MAR-2001; 2001JP-00083526
                                                                                       22-MAR-2001; 2001JP-00083526
                                                                                                                                                                                                                                                                                                                                                                                                                        1.46e-39
398.00
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87.5%
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(first entry)
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P-PSDB; ABP53725.
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 243 BP;
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JP2002272292-A.
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01-MAR-2000
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                                                                                                                                                                                                              Novel Brassica sp. derived protein having antimicrobial activity, useful for producing multiple disease resistant plants.
                                                                                                                                                                                                                                                                                      The invention comprises the amino acid and coding sequence of an antimicrobial protein obtained from Brassica sp. The DNA and protein sequences of the invention are useful in the production of a multiple disease resistant plant. The present DNA sequence encodes the Brassica antimicrobial protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGCCCAAGTTTGTGTCTATCATTGCCCCACTTTTTGCTGCTCTTGTTCTTTTAGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheGluhlaproThrMetValGluhlaGlnLysLeuCysGlnArgProSerGlyThrTrp
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 3; 16pp; Japanese
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                                                                            07-JUN-2004; 2004JP-00168986
                                                                                                          18-SEP-2001; 2001JP-00283117
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416.00
95.0%
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P-PSDB; ADU71303.
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Query Match:
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                 JP2004329215-A.
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                                              25-NOV-2004
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Zhu T;

Wang X,

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Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                            Claim 144; SEQ ID NO 2046; 577pp + Sequence Listing; English
           SCRIPPS RES INST.
SYNGENTA PARTICIPATIONS AG.
                                        Harper JF, Kreps J,
                                                           WPI; 2002-304127/34
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                                                                                                                                                                             The present sequence encodes an antibacterial protein isolated from Wasabia japonica. The antibacterial protein can be used as a food or feed additive. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                     An antibacterial protein gene of Wasabia japonica – useful as a food- or
feed-additive.
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                                                                                                                                                                                                                     Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;
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Mismatches:
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                                                                                                                                                          Claim 3; Page 12-13; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ14241 standard; DNA; 243 BP
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                      98JP-00121303
                                                         98JP-00121303
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                                                                                               WPI; 2000-057353/05.
P-PSDB; AAY57564.
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                                                                                                                                                                                                                                                                                 Best Local Similarity:
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 JP11313678-A
                                                          30-APR-1998;
                                      30-APR-1998;
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                   16-NOV-1999
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polymucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants. The method is useful in the production of transgenic plants end edged and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thalians stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TCAGGGGTTTGCGGAAACAGTAATGCATGCAAGAATCAGTGCATTAACCTTGAAGGAGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;
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69
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Mismatches:
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Job time : 455 secs
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394.00
93.8%
86.2%
89.3%
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Best Local Similarity:
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BN45.043G08F011229 BN45 Brassica napus CDNA clone BN45043G08, mRNA
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    (Dases 1 to 425)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infoblogen.fr).
Location/Qualifiers
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Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93, rue Henri Rochefort 91025 BVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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C083129
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CD834852.1 GI:32516792
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  CD834852 BN45.043G
CD833613 BN40.067P
CD833047 BN40.065M
CD83361 BN45.001C
CD828840 BN40.040A
CD83393 BN45.040A
CD829429 BN40.042B
                                                                  May 10, 2006, 06:02:00 ; Search time 3003.5 Seconds (without alignments) 1869.302 Million cell updates/sec
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1 MAKPASIIALLFAALVLFAA.....RHGSCNYVFPAHKCICYFPC
                                                                                                                                                                                                                             82156650
           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                 nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                          41078325 segs, 23393541228 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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9b_est2:**
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9b_est4:*
9b_est5:**
9b_est7:*
9b_est7:*
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Xgapop 10.0 , X
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Database :

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Result Š

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Total number

Searched:

Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

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CD833047 449 bp mRNA linear EST 10-JUL-2003 BN40.065M05F011229 BN40 Brassica napus cDNA clone BN40065M05, mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Fhis sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
                                                                                                                                                                                                              51 ATGGCTAAGTTTGCTTCCATCGTTGCCCTTCTTTTCTCTGCCCCTGGTTATTTTTGCTGCT
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Brassica napus
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Genoplante
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CD833047
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Genoplante.
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Contact: Genoplante
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Brassica napus
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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FEATURES

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CD833938
BN45.040A23F011018 BN45 Brassica napus cDNA clone BN45040A23, mRNA
CD828840
BN40.040A23F011019 BN40 Brassica napus cDNA clone BN40040A23, mRNA
                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermartophyta; Viridiplantae; Streptophyta; eudicotyledons; core eudicotyledons; roside; euroside II; Brassicales; Brassicaceae; Brassica. [ Loses 1 to 543)
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                                                                                                                                                                                                                                                                                        93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
Location/Qualifiers
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Contact: Genoplante
Genoplante
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BN45.001C04F010914 BN45 Brassica napus CDNA clone BN45001C04, mRNA
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                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. (bases 1 to 523)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Contact: Genoplante
Genoplante
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/tissue_type="seed"
/clone_lib="BN45"
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/cultivar="Jet Neuf"
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CD833661.1 GI:32515601
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Pred. No.:

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CN826227 413 bp mRNA linear EST 14-MAY-2005
EL1386 Brassica embryo library (EL) Brassica napus cDNA clone
EL1386 complete, mRNA sequence.
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11 (bases 1 to 413)
12 (bases 2 to 413)
13 (bases 3 to 413)
14 (bases 3 to 413)
15 (bases 4 to 413)
16 (bases 4 to 413)
17 (bases 4 to 413)
18 (bases 4 to 413)
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/dev stage="Mid to late embryos (4-6 mg)"
/lab_host="E. coli ElectroMAX DHS alpha-e (Invitrogen)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
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Molecular Genetics
Agriculture & Agri-Food Canada
107 Science Place, Saskatoon, Sakatchewan, Canada, S7NOX2
1Tel: 306 956 7247
Pax: 306 956 7247
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and http://genoplante-info.infobiogen.fr) Location/Qualifiers
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/cultivar="DH12075 (double )
                                                                    /organism="Brassica napus"
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/clone_lib="BN40"
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Matches:
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Seg primer: M13 Forward and T7.
Location/Qualifiers
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CN826227.1 GI:65296011
EST.
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Brassica napus
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Bequence.
CD829429
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( pases 1 to 646)
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                                                                                                                                         93, rue Henri Rochefort 91025 BVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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Contact: Genoplante
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                                                Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante Genoplante Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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/db_xref="taxon:3708"
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Brassica napus
  (bases 1 to 522)
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CD829429
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/clone_lib="Brassica embryo library (EL)"

(modified: GCGCCGCC*GACTAGTGAGCTC*cggacgcgtggGTCGAC);

(modified: GCGCCGCC*GACTAGTGAGCTC*cggacgcgtggGTCGAC);

Site 1: Not! Site 2: Sal1; Seeds were collected by Dr.

Francois Ouellet when they were still very green (mid to large stage, cotyledons were formed). The seed coats were removed and the remaining tissue was used for cDNA library construction. mRNA was poly-A primed using SuperScript Plasmid System cDNA Synthesis and Cloning kit (Invitrogen) After initial screened out using 22 oligos designed to match napins (including albumins), cruciferins, oleosins, trypsin inhibitor 2, cytosolic GAPDH, cyclophilins, HSP70, desaturase, and CAB (LHCP)."
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418 bp mRNA linear EST 10-JUL-200:
BN40.064A14F011227 BN40 Brassica napus cDNA clone BN40064A14, mRNA
equence.
CD832625.
CD832625.1 GI:32514565
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 418)
Genoplante.
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Unpublished (2003)
Contact: Genoplante
Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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CD833944 4 420 bp mRNA linear EST 10-JUL-2003
BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Location/Qualifiers
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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CD831111 421 bp mRNA linear EST 10-JUL-2003 BN40.058A09F011019 BN40 Brassica napus CDNA clone BN40058A09, mRNA sequence.
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Contact: Genoplante
Contact: Genoplante
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Fax: 33 1 69 47 54 10
Fax: 33 1 69 47 56 00
Fax: 30 1 60 47 50 10
Fax: 30 1 60 47
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              SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla
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CD833977
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BN25.064A05F020416 BN25 Brassica napus CDNA clone BN25064A05, mRNA
sequence.
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                                                                                289
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Unpublished (2003)
Contact: Genoplante
Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Fhis sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Gaps:
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                                          US-09-759-584-59 (1-80) x CD833944 (1-420)
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CD826491.1 GI:32508431
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Brassica napus
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CD827413 426 bp mRNA linear EST 10-JUL-2003
BN25.067G02F020123 BN25 Brassica napus CDNA clone BN25067G02, mRNA
sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosida II; Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 426)
Genoplante.
 1 (bases 1 to 422)
Genoplante.
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Umpublished (2003)
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Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Tel: 33 1 69 47 54 10
Tel: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
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Unpublished (2003)
Contact: Genoplante
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Conservative:
Mismatches:
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CD827413.1 GI:32509353
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CD833977 421 bp mRNA linear EST 10-JUL-2003 BN45.040D05F011019 BN45 Brassica napus cDNA clone BN45040D05, mRNA sequence.
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                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Vagnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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1-1: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante.info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                            Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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Matches:
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Mismatches:
Indels:
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and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
1. .426
1. .426
/organism="Brassica napus"
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Matches:
Conservative:
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Search completed: May 10, 2006, 09:42:56 Job time: 3006.5 secs

Title: Perfect score:

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Scoring table:

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AR207337 Sequence
AR642703 Sequence
AR642703 Sequence
AR614693 Sequence
AR612393 Sequence
AR6130280 Sequence
AR130280 Sequence
AR130281 Sequence
AR130280 Sequence
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X97318 R.sativus m
AX412329 Sequence
AX412502 Sequence
AX507351 Sequence
AX590057 Sequence
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AX412406 Sequence
AX412601 Sequence
AX651878 Sequence
AX651876 Arabidops
A68645 Sequence 13
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A68647 Sequence 15
AY063779 Arabidops
BD174928 Disease t
AF28180 Brassica
E31546 Antibacteri
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Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 05-DEC-1998
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AR014691 Sequence
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Patent: US 5773696-A 16 30-JUN-1998
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AY052236
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AR432392 Sequence
U18557 Raphanus sa
                                                                                May 10, 2006, 05:46:44 ; Search time 3626 Seconds (without alignments) 1881.195 Million cell updates/sec
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1 MAKFASIIALLFAALVLFAA.....RHGSCNYVFPAHKCICYFPC
          GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                     using frame plus p2n model
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Listing first 45 summaries
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Xgapop 10.0 , Xgapext
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Database :

Score

Result Š 4 4 4 2 4 4 2 2 2 2

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Chem. 267, 15301-15309"
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Terras, F.R.G., Eggermont, K., Kovaleva, V., Raikhel, N.V.,
Osborn, R.W., Kester, A., Rees, S.B., Torrekens, S., Van Leuven, F.,
Vanderleyden, J., Cammue, B.P.A. and Broekaert, W.F.
Small cysteine-rich antifungal proteins from radish: their role in
                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (14-DBC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
On Feb 9, 1995 this sequence version replaced gi:609321.
Location/Qualifiers
                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
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Matches:
Conservative:
Mismatches:
Indels:
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Plant Cell 7, 568-573 (1995)
2 (bases 1 to 395)
                                                                         Raphanus sativus (radish)
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1 (bases 1 to 285)
Liangju,, Shah,D.M., Wu,Y.S. and Rosenberger,C.A.

Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi
Patent: US 6652280-A 16 25-NOV-2003;
Monsanto Technology LLC; St. Louis, MO
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Sequence 16 from patent US 6653280.
AR432392
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                                                       US-09-759-584-49 (1-80) x AR014692 (1-285)
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   Dubock, A.C., Fowell, K.A. and Rees, S.B.
ANTIMICROBLAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
PALENT: NO 9416076-A 37 21-JUL-1994;
ZENECA LTD (GB)
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PARTHER, WO 9721814-A 19 19-JUN-1997;
ZENECA LTD (GB)
Other publication AU 1105397 19970703.
Location/Qualifiers
1. 414
/organism="unidentified"
/mol type="unassigned DNA"
/db_xref="taxon:32644"
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                                                  Other publication AU 5820494 940815.
Location/Qualifiers

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    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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Sequence 19 from Patent WO9721814.
A63404
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I (bases I to 414)
Brockaert, W.F., Cammue, B.P.A., Terras, F.R.G., Vanderleyden, J., Osborn, R.W. and Rees, S.B.
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/mol_type="unassigned DNA"
/db xref="taxon:3726"
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ICI PLC (GB)
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Sequence 37 from Patent WO9416076.
A39549
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Raphanus sativus
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unidentified
unclassified sequences.
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R.sativus AFP1 gene.
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RESULT 5 A39549 LOCUS

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1 (bases 1 to 414)

Brockent W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,

Terras, F.R.G. and Vanderleyden, J.

Blocidal proteins

Patent: 19.5385.5-4 48 23-JUL-1996;

Location/Qualifiers
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Terras, F.R.G. and Vanderleyden, J.
Biocidal proteine
Patent: US 6187904-A 48 13-FEB-2001;
Location/Qualifiers
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Sequence 48 from patent US 5538525.
123728 123728.1 GI:1603598
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16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
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1 (bases 1 to 414)
Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
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Sequence 48 from patent US 6187904.
AR130272.1 GI:14118169
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TITLE JOURNAL FEATURES

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REFERENCE AUTHORS 255

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ORGANISM

REFERENCE AUTHORS

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ES Location/Qualifiers ource 1414 /organism="unknown" /mol_type="genomic DNA" ent Scores: 1.08e-44 Length:	Score: 442.00 Matches: 80 Percent Similarity: 100.04 Conservative: 0 Beet Local Similarity: 100.04 Mismatches: 0 Query Match: 100.04 Indels: 0 DB: 6 US-09-759-584-49 (1-80) x AR374914 (1-414)	Oy 1 MetalaLysPhealaSerIleIleAlaLeuDealaAlaLeuValLeuPheAlaAla 20	Db 76 TTCGAAGCACCAACAATGGTGGAAGCACAAGAGGCCAAGTGGGAATGGTGGTGTGTGT	Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80	RESULT 12 AR642703 LOCUS AR642703 AR642703 AR642703 A14 bp DEFINITION Sequence 19 from patent US 6864068. ACCESSION AR642703 ACCESSION AR642703	S . Unknown. ISM Unknown. Unclassified.	REFERENCE 1 (bases 1 to 414) AUTHORS Rees, S.B., De Samblanx, G.W. and Broekaert, W.F. TITLE Antifungal proteins JOURNAL PATENT: US 684066 A 19 08-MAR-2005;	GBX; Location/Qualifiers FEATURES 1. 414 Source //wranien-linkboom"		Alignment Scores: 1.08e-44 Length: 414 Pred. No.: 1.08e-44 Length: 414 Score: 442.00 Matches: 80 Percent Similarity: 100.0\$ Conservative: 0 Best Local Similarity: 100.0\$ Mismatches: 0 Query Match: 100.0\$ Indels: 0 DB: 6	-09-759-584-49 (1-80) x AR642703 (1-414)	Qy 1 MetalaLysPhealaSerIleIleAlaLeuLeuPhealaAlaLeuValLeuPheAlaAla 20	Oy 21 PheGlualaProThrMetValGlualaGlnLysLeuCysGluArgProSerGlyThrTrp 40	41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCyslleAsnLeuGluLysAla 60
Qy 41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60 Db 136 TGGGAGTCTGTGGAAACAATGATGAGGATCAGTGCATTAACCTTTTTTTT	RESULT 10 AR207337 LOCUS LOCUS DEPINITION Sequence 19 from patent US 6372888. ACCESSION AR207337 VERSION AR207337.1 GI:21506219	SOURCE Unknown. SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 414) AUTHORS De Samblanx, G.Wivina., Broekaert, W.Frans. and Rees, S.Bronwen.	JOHENAL Patent: US 6372888-A 19 16-APR-2002; PEATURES Location/Qualifiers source /organism="unknown" /mol_type="unassigned DNA"	Length:	Scole: Secont Similarity: 100.0% Conservative: 0 Best Local Similarity: 100.0% Minmatches: 0 Query Match: 100.0% Indels: 0 DB: 6 Gaps: 0	PheAlaSerile	4 4	Qy 41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60	Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80 Db 196 CGACATGCATCTTGCAACTATGTCTTCCCAGCTCAAAGTGTATCTGCTACTTTCCTTGT 255	RESULT 11 AR374914 LOCUS LOCUS DEFINITION Sequence 45 from patent US 6605698. ACCESSION AR374914 VERSION AR374914.1 GI:40077932	SM	Unclassified. REFERENCE 1 (bases 1 to 414) AUTHORS Van Amerongen, A., Fant, F., Borremans, F.A., De Samblanx, G.W.,	Siftsma, L., Meloen, R.H., Puijk, W.C., Schaaper, W.M., Brockaert, W.F., van Gelder, W.M.J. and Rees, S.B. TITLE Antifungal peptides and composition thereof JOURNAL Patent: US 6605698-A 45 12-AUG-2003,	

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PAT 05-MAR-1997
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unclassified sequences.
unclassified sequences.
bubock, A.C., Powell, K.A. and Rees, S.B.
Dubock, A.C., Powell, K.A. and Rees, S.B.
ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
PATENT: WO 9416076-A 41 21-UUL-1994;
ZENECA LID (GB)
Other publication AU 5820494 940815.
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Sequence 41 from Patent WO9416076.
A39553.1 GI:2295844
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I (bases 1 to 285)
Liang, J., Shah, D. Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
                                                                                                  PAT 05-DEC-1998
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                                SM Unknown.
Unclassified.

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SE I (bases 1 to 285)

RS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.

Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi

NAL Patent: US 6653280-A 17 25-NOV-2003;

Monsanto Technology LLC; St. Louis, MO

Location/Qualifiers

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Patent: US 5773696-A 17 30-JUN-1998;
Location/Qualifiers
1. 285
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/mol_type="unassigned DNA"
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Sequence 17 from patent US 5773696.
AR014693.1 GI:3972147
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Sequence 17 from patent US 6653280.
AR432393.1 GI:40194670
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Abz42136 Arabidops
Aav10633 A. thalia
Aaz75091 Arabidops
Aav10633 A. thalia
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Aag87923 A. thalia
Aac9928 A. thalia
Aac94582 Amplified
Aat94582 Amplified
Aat94581 Composite
Aac94584 Arabidops
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Adc51223 Brassica
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Aaz99325 DNA encod
Aaz99326 DNA encod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                                                                                                     Aaz99324
Aaz99333
                                                                                                                                                                                                                                                                                                                                                                        Aaz99334
                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                        AAV10633
ABQ82691
ABQ82691
ABQ82691
ABQ82728
ABG87728
AAT94574
AAT94582
AAT94582
AAT94584
AAT94581
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AAT94281
                                                                                                                                                                                                                                                                                                                                                                                 AAZ51396
AAZ99325
AAZ99326
ADR39326
         AAQ70130
ADC51221
ADU71300
                                     ADC51223
ADU71302
AAA53190
AAZ99339
ABQ82690
AAZ39123
ABZ14241
ADG87651
ADG87651
ADG87621
                                                                                                                                                                                                                                                                                                                                 ADG32348
                                                                                                                                                                                                                                                                                                                     ADG32350
                                                                                                                                                                                                                                                                                                                                        AAZ99327
AAZ99324
AAZ99333
AAZ99334
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16. .256
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ38650 standard; DNA; 414 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91GB-00018523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                                                             Raphanus sativus.
                                                                                                                                                               91.0
91.0
889.8
899.8
899.8
7.2
899.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rs-AFP1 CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9305153-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
07-JUL-1993
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                                                                                                                                                                                                                397
396.5
396.5
396.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
AAQ38650
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                                                                                                                                                                                                                                                                                                                              Aaq38650 Rs-AFP1 c
Aaq70128 Antimicro
Aat72333 Raphanus
Aat68696 Radish an
                                                                  May 10, 2006, 05:44:15 ; Search time 452 Seconds (without alignments) 1769.387 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                               1 MAKFASIIALLFAALVLFAA......RHGSCNYVFPAHKCICYFPC
         GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                                                                  4996997 segs, 3332346308 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ38650
AAQ70128
AAT72333
AAT68696
                                                                                                                                                  BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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4 4 4 4
2 2 2 2
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Database :

Result No.

Total number

Searched:

DNA encod DNA encod DNA encod DNA encod

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Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPI from R. sativus. The full-length cDNA sequence of Rs-AFPI is given in AAQ70128. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antifungal protein; candida; fungal resistance; food additive; radish;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 Trceaagcaccaacaardergeaagcacaagaagrrergegaaagccaaagreeacarge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla
                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheGlualaProThrMetValGlualaGlnLysLeuCysGluargProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                    SB;
                                                                                                                                                                                94WO-GB000012.
                                                                                                                                                                                                                                                                                                    Rees
                                                                                                                                                                                                                     93GB-00000281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT72333 standard; cDNA; 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .04e-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 31; 39pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442.00
100.0%
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(first entry)
                                                                                                                                                                                                                                                                                                    Dubock AC, Powell KA,
                                                                                                                                                                                                                                                                                                                                         WPI; 1994-249223/30.
P-PSDB; AAR57325.
                                                                                                                                                                                                                                                            (ZENE ) ZENECA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                            Raphanus sativus.
                                                                                                                                                                                05-JAN-1994;
                                                                                                                                                                                                                       08-JAN-1993;
                                                                                                   WO9416076-A1
                                                                                                                                          21-JUL-1994.
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19-JAN-1998
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                                                                                                                                                                                                                                                                                                                This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and olosyigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII CDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage (C their size compared by agarose gel electrophoresis. Four clones had inserts sizes of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAAAAGCA 195
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                                                                                                                                                                                                  Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The longest sequence is given here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetalaLysPhealaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerGlyValCysGlyAsnAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla

        ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
                                                                                                   Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                   Osborn RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-759-584-49 (1-80) x AAQ38650 (1-414)
                                                                                                                                                                                                                                                                                 Example 21; Fig 35; 110pp; English.
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                                                          (ICIL ) IMPERIAL CHEM IND PLC
  92GB-00003038.
92GB-00013526.
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                                                                                                   Cammue BPA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
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                                                                                                                                                             WPI; 1993-100978/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                      Vanderleyden J;
                                                                                                   Broekaert WF,
  13-FEB-1992;
25-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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14-FEB-1995
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(first entry)

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CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                        136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                                                        61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
                                                                                                                                                                                                                                                                                                                                Rs-AFP1; radish antifungal protein 1; fungicide; salt tolerance;
preservative; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                                             Radish antifungal protein 1 (Rs-AFP1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 39pp; English.
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                                                                                                                                                                                     AAT68696 standard; cDNA; 414
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P-PSDB; AAW19617.
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                                                                                                                                                                                                                                                                                                                                                                                       Raphanus sativus.
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                                                                                                                                                                                                                                                         13-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9721814-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1997.
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   41
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAAGGCCAAGTGGGAAATGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheGlualabroThrWetValGluAlaGlnIysLeuCysGluArgProSerGlyThrTrp 40
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crop protection; plant defensin; bacterial protection; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetalalysPhealaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Amerongen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA sequence encodes an Rhapanus sativus (radish) antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sijtsma L, Van Amerong
Borremans FAM, Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                           (pos:85. .87, aa:Glu)
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Puijk WC, Schaaper WMM,
, Samblanx GW, Fant F,
                                                                        Location/Qualifiers
16. .258
                                                                                                                               except=
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                                                                                                                                                                                                                                                                                                                                                                  95GB-00025455
96GB-00006552
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P-PSDB; AAW19280.
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                                    Raphanus sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meloen RH, Puij)
Broekaert W, Sa
Van Gelder WMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                         WO9721815-A2
                                                                                                                                                                                                                                                                                                                                12-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                  13-DEC-1995;
28-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                              sig_peptide
                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                             19-JUN-1997
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Rees SB

96WO-GB003065. 95GB-00025474

/transl_except= (pos:85. .87, aa:Glu)

/*tag= b 103. .255 /*tag= c

location/Qualifiers

.6. .258

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This cDNA clone codes for the preprotein for radish antifungal protein 1 (Rs-AFP1) (AAW19617). Novel antifungal proteins are based on Rs-AFP1, Rs-AFP2 (see AAW19615), Rs-AFP3 and Rs-AFP4, especially those in which Gly9 is repaced by Arg, Vsl) by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW12371-90) of Rs- AFP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
                                                                                                                                                                                                       Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
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Mismatches:
Indels:
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Matches:
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Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; PCR; polymerase chain reaction; mutagenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAGACTTGAGAAAGCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the 4 largest clones were then sequenced and found to differ only in the length of their 5' and 3' UTR's. The longest sequence was identified as Rs-AFP1 (AAQ38650). Rs-AFP2 was seen to differ by only 2 amino acids from Rs-AFP1, so the Rs-AFP1 cDNA was transformed to the Rs-AFP2 nucleotide sequence by PCR assisted site directed mutagenesis. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                          16 ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                               MetalaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla
                                                                                                                                                       Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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433.00
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial Rs-AFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-249223/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                    Alignment Scores:
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14-FEB-1995
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA represents the sequence of Rs-AFP2 from Raphanus sativus. PCR screening a Raphanus sativus ded together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and digoxigenin-11-dTPP instead of dTTP to give a digoxigenin-11-dTPP instead of dTTP to give a digoxigenin-13-dTPP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ plaque were principled and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage the AROB-Inserts from 22 postitive clones were excised by Economack by agarces gel electrophoresis. Four clones had insert sizes of approx. 400bp the others between 250-300bp. The inserts
                                                                                                                                                                                                                                                                                         255
                                                                                                               TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
                                                                                                                                                                                                  TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 195
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                                                                                                                                                                                                                                            ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                   SerglyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla
                                                                         PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rees SB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
16. .256
/*tag= a
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92GB-00003038.
92GB-00013526.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-1991;
13-FEB-1992;
25-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RB-AFP2 CDNA
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07-JUL-1993
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Disclosure; Page 33; 39pp; English.

diseases.

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DB:
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ID ADU7
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Plant-derived antimicrobial proteins are expressed in endosymbiotic clavibacter xyll subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length CDNA sequence of PCR assisted site-directed mutagenesis of Rs-AFP2 is given in AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                       ATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTGTTCTTTTTGCTGCT
                                                                                                                                                                                                                                                              TTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCCCAAAGGCCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                            SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla
                                                                                                                                                                                                                                                                                                                                    ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT
                                                                                                                                                                                                                                                  PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                         TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGGATTAGACTTGAGAAAGCA
                                                                                                                                                                                                          MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
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/product= "Brassica oleracea defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antimicrobial protein; defensin; transgenic plant; composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                   Other
                                                                                                                 288
78
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                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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1. .243
/*tag= a
                                                                                  288 BP; 70 A; 66 C; 69
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433.00
98.8%
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P-PSDB; ADC51222.
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                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                                     Alignment Scores:
Pred. No.:
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                                                                                   Sequence
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plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
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                                                                                                                The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
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Matches:
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                                                                       Claim 3; SEQ ID NO 1; 34pp; Japanese
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                 Novel Brassica sp. derived protein having antimicrobial activity, useful for producing multiple disease resistant plants.
                                                             The invention comprises the amino acid and coding sequence of an antimicrobial protein obtained from Brassica sp. The DNA and protein sequences of the invention are useful in the production of a multiple disease resistant plant. The present cDNA sequence encodes the Brassica oleracea defensin protein.
                                                                                                                                                                                                                                                 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                         G; 125 T; 0 U; 0 Other;
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Matches:
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                                            Example 2; SEQ ID NO 1; 16pp; Japanese.
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/*tag= a
/product= "Brassica d
                                                                                                                         Seguence 394 BP; 116 A; 71 C; 82
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P-PSDB; ADU71301
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Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
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                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease restance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
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                                                                                                                                                               Claim 3; SEQ ID NO 3; 34pp; Japanese
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WPI; 2003-621123/59.
P-PSDB; ADC51224.
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Best Local Similarity:
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161 TCAGGAGTCTGTGGAAATAATAACGCATGCAAGAATCAGTGCATTCGACTTGAGAAAGCA 220
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protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
                 Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.
                                                                                                              The present sequence encodes an antibacterial protein, designated radishin, isolated from Raphanus sativus (radishi). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and rice blast disease against pathogenic microbes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
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/*tag= a /*tag= a /product= "fusion protein of DmAMP1 and RsAFP2"

                                                                                                                                                                                                 Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                 Claim 1; Page 4; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ99339 standard; DNA; 575 BP
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98GB-00026753
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                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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Unidentified.
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04-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
                                                                                                             Novel Brassica sp. derived protein having antimicrobial activity, useful for producing multiple disease resistant plants.
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                                                                                                                                                                                              The invention comprises the amino acid and coding sequence of an antimicrobial protein obtained from Brassica sp. The DNA and protein sequences of the invention are useful in the production of a multiple disease resistant plant. The present DNA sequence encodes the Brassica antimicrobial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCCAAGTTTGTGTCTATCATTGCCCCACTTTTTGCTGCTCTTGTTTTAGCTGCT
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pathogenic microbe; radish; rice blast disease; ds.
                                                                                                                                                                                                                                                                                                  Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
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                               (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
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Matches:
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                                                                                                                                                                 Claim 3; SEQ ID NO 3; 16pp; Japanese.
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18-SEP-2001; 2001JP-00283117
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P-PSDB; AAY91117.
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Best Local Similarity:
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01-MAR-2000
                        24-SEP-2002.
                                                                                                                                                                                                                                                                                   invention
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                                                                                                                 The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) I and the antifungal protein 2 (RBAFP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one considic and one basic residue as a cleavable linker sequence
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                                                          Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetalalysPhealaSerIleIlealaLeuLeuPhealaAlaLeuValLeuPhealaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wasabia japonica, gamma-thionin; plant; disease-resistant plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGCTAAGTTTGCGTCCATCATCGCCCCTTTTTGCTGCTCTTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
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                                                                                                                                                                                                                                                                                                         Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;
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 Evans IJ,
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/product= "gamma-thionin"
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1. .243
                                                                                               Disclosure; Fig 34; 151pp; English
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 Broekaert WF, Francois IEJA,
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418.00
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                        WPI; 2000-246564/21.
P-PSDB; AAY84072.
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The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Eutrema wasabi (Wasabia japonica) gamma-thionin protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TTTGAAGCACCATCAATGGTGGAAGCGCAGAAGTTGTGCGAGAAAGTCAAGTGGGACATGG 120
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                                                                                                                                                                                                                          18
                                                                                                                                                                                                                       A disease-resistant plant in which wasabi gamma-thionin gene introduced, creation of the disease-resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;
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/product= "antibacterial protein"
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                                                                                                                                                                                                                                                                                                      Claim 3; Page 8; 11pp; Japanese.
22-MAR-2001; 2001JP-00083526
                                               22-MAR-2001; 2001JP-00083526
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Wang X, Zhu T;

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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polymucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arrabidopsia thallana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence
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                                                                                                             Identifying a stress condition to which a plant cell has been expose producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                  information supplied to Derwent by the Buropean Patent Office
                                                                                                                                                           Claim 144; SEQ ID NO 2046; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;
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Job time : 453 secs
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SYNGENTA PARTICIPATIONS AG
                                                         Harper JF, Kreps J,
                                                                                     WPI; 2002-304127/34
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                                                                                                                                                                                                                                                           The present sequence encodes an antibacterial protein isolated from Wasabia japonica. The antibacterial protein can be used as a food or feed additive. (Updated on 15-SEP-2003 to standardise OS field)
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                                                                                                                                                                                An antibacterial protein gene of Wasabia japonica - useful as a food- or feed-additive.
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                                                                                                                                                                                                                                                                                                                      Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                   Claim 3; Page 12-13; 16pp; Japanese.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-2001; 2001WO-US026685
                                                         98JP-00121303
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407.00
96.2%
90.0%
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                                                                                                                                             2000-057353/05
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Best Local Similarity:
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                                                                                                                  (IWAT-) IWATE
                                                                                     30-APR-1998;
 JP11313678-A
                                                         30-APR-1998;
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                           16-NOV-1999
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Conservative: Mismatches: Indels: Length: Matches:

1.59e-41 403.00 95.0% 88.8%

Gaps:

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OM protein

Run on:

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LI1366 Brassica embryo library (EL) Brassica napus cDNA clone
EL1386 complete, mRNA sequence.
CD827413 BN25.067G
CD831294 BN40.058N
CD831409 BN40.058N
CD834008 BN45.040E
CN72661 3ETMS_UP
CD828332 BN25.070H
CD831014 BN40.047K
CD831019 BN45.040I
CD834090 BN45.040I
CD834090 BN45.040I
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CN72634 3ETMS_UP
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CN72632 BN46.067P
DN778122 ENG9 CG7P
DN778122 ENG9 CG7P
CN83613 BN40.067P
CN72625 3ETMS_UP
CN827131 BN40.067B
CD833048 BN46.064B
CD833048 BN46.064B
CD833048 BN46.062B
CN827135 BL20499 FB
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1 (bases 1 to 413)
Sharpe, A.G., Gjetvaj, B., Durkin, J. and Lydiate, D.J.
Brassica napus ESTS
Unpublished (2004)
Contact: Sharpe, A.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Brassica napus"
/mol type="mRNA"
/cultivar="DH12075 (double haploid line from Cresor x
/westar cross)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agriculture & Agri-Food Canada
107 Science Place, Saskatoon, Sakatchewan, Canada, S7NOX2
1981: 306 956 7271
Fax: 306 956 7247
Email: sharpeadagr.gc.ca
Seq primer: M13 Forward and T7.
  CD827413
CD831294
CD831294
CD831294
CN726641
CN726641
CD83131014
CD83131704
CD8314090
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CN826227.1 GI:65296011
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CD832625 BN40.064A
CD833944 BN45.040B
CD826491 BN25.064A
CD831317 BN45.040B
CD833977 BN45.040B
                                                                                        May 10, 2006, 06:02:00 ; Search time 3003.5 Seconds (without alignments) 1869.302 Million cell updates/sec
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                                                                                                                                                                    MAKFASIIALLFAALVLFAA......RHGSCNYVFPAHKCICYFPC
                 GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                                                                  nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                         41078325 segs, 23393541228 residues
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Maximum Match 100%
Listing first 45 summaries
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CD832625
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CD826491
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CD833983
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Database :

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Result Š

Total number

Searched:

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CD833944 420 bp mRNA linear EST 10-JUL-2003
BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93, rue Henri Rochefort 91025 BVRY CEDEX France
193, rue Henri Rochefort 91025 BVRY CEDEX France
194 1 54 00

Fax: 33 1 69 47 54 00

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante.info.infobiogen.fr).

Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/clone_lib="BN40"
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/cultivar="Jet Neuf"
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Brassica napus
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/dev stage="Mid to late embryos (4-6 mg)"
/lab_host="E. coli ElectroMAX DH5 alpha-e (Invitrogen)"
/clone llb="Brassica embryo library (EL)"
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(modified: GCGCCGCC-GACTAGTGACCTC-eggacgcgtgGTCGAC);
Site 1: Not1; Site 2: Sal1; Seeds were collected by Dr.
Francois Ouellet when they were still very green (mid to large stage, cotyledons were formed). The seed coats were removed and the remaining tissue was used for cDNA library construction. mRNA was poly-A primed using SuperScript Plasmid System cDNA Synthesis and Cloning kit (Invitrogen) After initial screening, the most abundant redundant clones were screened out using 22 oligos designed to match napins (including albumins). cruciferins, oleosins, HSP70, desaturase, and CAB (LHCP)."
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CD832625
CD832625.1 GI:32514565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 CTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAGAGGCCAAGTGGGACATGG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 SerGlyValCysGlyAsnAsnAsnAsaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Finis sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infoblogen.fr).
Location/Qualifiers
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Contact: Genoplante
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    db_xref="taxon
clone="EL1386"
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Brassica napus
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RESULT 2 CD832625

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21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgPrc	n napus cDNA cophyta; Emb dicotyledon ; Brassicac french prog	e e	ent Scor No.: t Simile ocal Sin Match:	Oy 1 MetalalysPhealaSerIleIleAlaLeuLeuPhealaAlaLeuValLeuPhealaAla 20 51 ATGGCTAAGTTTGCTTCCATCGTTTTTTGCTGCTCTTTTGGTGCTTTTTGGTGCTTTTTGGTGCTTTTTGGTGCTTTTTGGTGCTTTTTGGTGCTTTTTT
Matches: 79 Matches: 79 St. 00 Matches: 79 Conservative: 0 St. Local Similarity: 98.8\$ Mismatches: 1 St. Match: 98.6\$ Mismatches: 1 St. Match: 98.6\$ Mismatches: 0 Gaps: 0 Gaps: 0 Conservative: 0 Gaps: 0 Conservative: 0 MetalalysphealaSerIleIlealaLeuLeuPhealaalaalaalaalaalaalaalaalaalaalaalaala	Qy 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60 Db 170 TCAGGAGTCTGGAAACAATGCATGCAGATCAACTTGAGAAAGCA 229 Qy 61 ArGHISGLYSECYSASNTYVAlPheProAlaHiSLYSCYSILECYSTYPPheProCys 80 Db 230 CGACATGGATCTTGCAACTTCCCAGCTCACAGTGTATTTGCTACTTCCTTGT 289 RESULT 4 CD826491 LOCUS 421 bp DBFINITION BN25.064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA ACCRSSION CD826491	Σ	### ##################################	Alignment Scores: Alignment Scores: Pred. No.: Score: Score: Best Local Similarity: 98.6\$ Mismatches: 0 Conservative: 98.6\$ Mismatches: 1.69e-41 Length: 79 Best Local Similarity: 98.6\$ Mismatches: 0 Gaps: 0.09-759-584-49 (1-80) x CD826491 (1-421) Qy

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CD827413 426 bp mRNA linear EST 10-JUL-2003 BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 426)
Genoplante.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosida II, Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                   93. The Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Flax: 31 69 47 54 10
plant genounce has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Contact: Genoplante
Genoplante
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93, rue Henri Rochefort 91025 EVRY CEDEX France
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                                                                    CD833977 421 bp mRNA linear EST 10-JUL-2003 BN45.040D05F011019 BN45 Brassica napus CDNA clone BN45040D05, mRNA
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   231 CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATTTGCTACTTCCCTTGT 290
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193, The Henri Rochefort 91025 BVRY CEDEX France
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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Brassica napus (rape)
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CD833977.1 GI:32515917
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 438)

Genoplante.
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Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
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Unpublished (2003)
Contact: Genoplante
Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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CD831294.1 GI:32513234
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CD831479 438 bp mRNA linear EST 10-JUL-2003
BN40.059J13F011208 BN40 Brassica napus CDNA clone BN40059J13, mRNA
sequence.
CD831479
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Genoplante.
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Location/Qualifiers
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Contact: Genoplante Genoplante Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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3ETW. 16 003 H02_10JUN2003_001 Brassica napus 3ETMS Brassica napus CN726424
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                                             171 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 230
                                                                                                    1. .453
/organism="Brassica napus"
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Sfi1B; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."
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L Unpublished (2004)
Contact: Bd Tsang
Contact: Bd Tsang
Plant Natural Products
National Research Council of Canada
National Research Council of Canada
Saskatchewan, 57N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Email: Bd Tsang@mrc-cnrc.gc.ca
High quality sequence stop: 453.
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                   SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla
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Brassica napus
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Brassica napus
Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids; eurosids II, Brassicales; Brassicaceae; Brassica.
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Gaps:
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                        CN726661 CN726661 456 bp mRNA linear EST 14-MAY-2005 3ETMS UP_006 G02_10JUN2003_002 Brassica napus 3ETMS Brassica napus cDNA 5', mRNA sequence.
CN72661.1 GI:65284463
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BN25.070H07F020125 BN25 Brassica napus CDNA clone BN25070H07, mRNA
sequence.
CD828332.1 GI:32510272
EST.
Brassica napus (rape)
                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="Brassica napus 3ETMS"
/note="Vector: pDNR-LIB_CREATOR; Site_1: SfilA; Site_2: SfilB; Sequences have been trimmed to remove vector and low quality regions using LUCY sequence cleanup software incr ora
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      MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla

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                                                                                                                                                                                                                                                                                Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4819
Fax: 306 975 4819
Fax: 307 975 4819
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Fax: 4819
Figh quality sequence stop: 456.
Location/Qualifiers
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Contact: Ed Tsang
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National Research Council of Canada
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/db_xref="taxon:3708"
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CN726661
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CD831014 553 bp mRNA linear EST 10-JUL-2003
BN40.047K12F011228 BN40 Brassica napus CDNA clone BN40047K12, mRNA
Brassica napus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosida, eurosida II, Brassicales, Brassicaceae; Brassica.
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                                                                                                                                                                                                                                           93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infoblogen.fr).
Location/Qualifiers
                                                                                                                                          Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
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Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 AIGGCTAAGTITIGCTITCCATCATIGCCCTACTITITITIGCTGCTCTGGTCCTTTTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 TCAGGAGTCTCTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATTTGCTACTTCCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetalalysPhealaSerIleIleAlaLeuLeuPhealaAlaLeuValLeuPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
Gaps:
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/tissue_type="seed"
/clone_lib="BNS5"
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Matches:
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436.00
98.8%
98.8%
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Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers

L. 553

/organism="Brassica napus"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN40047K12"
/tissue type="seed"
/clone_lib="BN40"
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                                                                                                                                                                                                                                                                                                                                                                                                           110 CTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAGAGGCCAAGTGGGACATGG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289
                                                                                                                                                                                                                                                                                                                                                                                         21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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DB:
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